



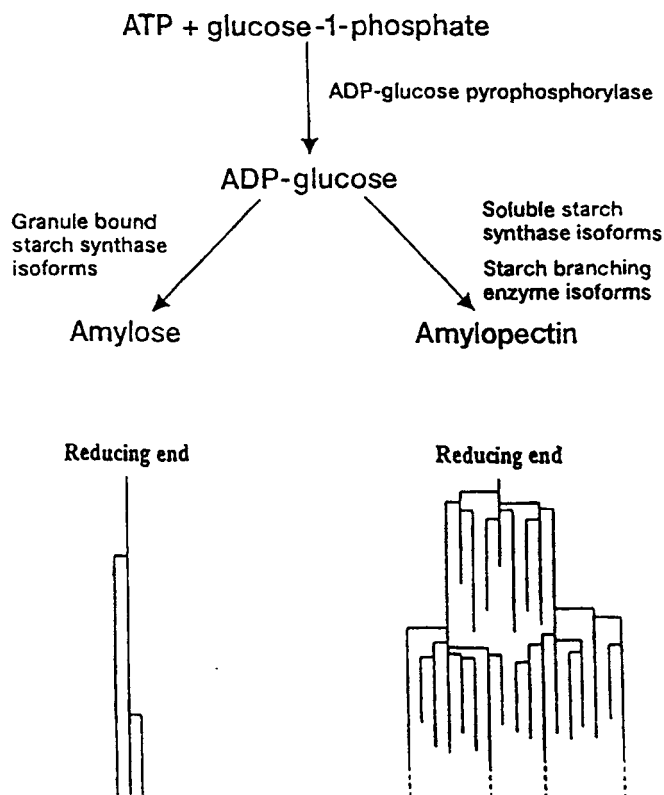
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(54) Title: ANTISENSE INTRON INHIBITION OF STARCH BRANCHING ENZYME EXPRESSION

(57) Abstract

A method of inhibiting gene expression is described. The method, which affects enzymatic activity in a plant, comprises expressing in a plant (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence codes, partially or completely, for an intron in an antisense orientation of a class A SBE; and wherein the nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.



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ANTISENSE INTRON INHIBITION OF STARCH BRANCHING ENZYME EXPRESSION

The present invention relates to a method of inhibiting gene expression, particularly inhibiting gene expression in a plant. The present invention also relates to a nucleotide
5 sequence useful in the method. In addition, the present invention relates to a promoter that is useful for expressing the nucleotide sequence.

Starch is one of the main storage carbohydrates in plants, especially higher plants. The structure of starch consists of amylose and amylopectin. Amylose consists essentially of straight chains of α -1-4-linked glycosyl residues. Amylopectin comprises chains of
10 α -1-4-linked glycosyl residues with some α -1-6 branches. The branched nature of amylopectin is accomplished by the action of *inter alia* an enzyme commonly known as the starch branching enzyme ("SBE"). SBE catalyses the formation of branch points in the amylopectin molecule by adding α -1,4 glucans through α -1,6-glucosidic branching linkages. The biosynthesis of amylose and amylopectin is schematically shown in Figure
15 1, whereas the α -1-4-links and the α -1-6 links are shown in Figure 2.

In Potato, it is known that two classes of SBE exist. In our copending international patent applications PCT/EP96/03052 and PCT/EP96/03053, class B potato SBE and a gene encoding it are discussed. In international patent application WO96/34968, class A potato SBE and a cDNA encoding it are disclosed.

20 It is known that starch is an important raw material. Starch is widely used in the food, paper, and chemical industries. However, a large fraction of the starches used in these industrial applications are post-harvest modified by chemical, physical or enzymatic methods in order to obtain starches with certain required functional properties.

Within the past few years it has become desirable to make genetically modified
25 plants which could be capable of producing modified starches which could be the same as the post-harvest modified starches. It is also known that it may be possible to prepare such genetically modified plants by expression of antisense nucleotide coding sequences. In this regard, June Bourque provides a detailed summary of antisense strategies for the genetic manipulations in plants (Bourque 1995 Plant Science 105 pp 125-149). At this
30 stage, reference could be made to Figure 3 which is a schematic diagram of one of the proposed mechanisms of antisense-RNA inhibition.

In particular, WO 92/11375 reports on a method of genetically modifying potato so as to form amylose-type starch. The method involves the use of an anti-sense construct that can apparently inhibit, to a varying extent, the expression of the gene coding for formation of the branching enzyme in potato. The antisense construct of WO 5 92/11375 consists of a tuber specific promoter, a transcription start sequence and the first exon of the branching enzyme in antisense direction. However, WO 92/11375 does not provide any antisense sequence data. In addition, WO 92/11375 only discloses the use of the potato GBSS promoter.

WO 92/14827 reports on a plasmid that, after insertion into the genome of a plant, 10 can apparently cause changes in the carbohydrate concentration and carbohydrate composition, such as the concentration and composition of amylose and amylopectin, in the regenerated plant. The plasmid contains part of the coding sequence of a branching enzyme in an antisense orientation.

EP-A-0647715 reports on the use of antisense endogenous mRNA coding DNA to 15 alter the characteristics and the metabolic pathways of ornamental plants.

EP-A-0467349 reports on the expression of sequences that are antisense to sequences upstream of a promoter to control gene expression.

EP-A-0458367 and US-A-5107065 report on the expression of a nucleotide sequence to regulate gene expression in a plant. The nucleotide sequence is 20 complementary to a mRNA sequence of a gene and may cover all or a portion of the non-coding region of the gene. In other words, the nucleotide sequences of EP-A-0458367 and US-A-5107065 must at least comprise a sequence that is complementary to a coding region. EP-A-0458367 and US-A-5107065 contain minimal sequence information.

WO96/34968 discusses the use of antisense sequences complementary to 25 sequences which encode class A and class B potato SBE to downregulate SBE expression in potato plants. The sequences used are complementary to SBE coding sequences.

Kuipers *et al* in Mol. Gen. Genet. [1995] 246 745-755 report on the expression of a series of nucleotides that are antisense to part of the genomic intron sequences of potato granule bound starch synthetase. Here the antisense intron sequences are attached to a 30 part of the antisense exon sequences - wherein the intron sequences and the exon

sequences are naturally associated with each other. In addition, the expressed antisense intron sequences are at most 231 bp in length.

Likewise, Kull *et al* in J. Genet. & Breed. [1995] 49 69-76 report on the expression of a series of nucleotides that are antisense to part of the genomic intron sequences of potato granule bound starch synthetase. Likewise, here the antisense intron sequences are attached to a part of the antisense exon sequences - wherein the intron sequences and the exon sequences are naturally associated with each other. In addition, likewise, the expressed antisense intron sequences are at most 231 bp in length.

Shimada *et al* in Theor. Appl. Genet. [1993] 86 665-672 report on the expression of a series of nucleotides that are antisense to part of the genomic intron sequences of rice granule bound starch synthetase. Here the antisense intron sequences are attached to a part of the antisense exon sequences - wherein the intron sequences and the exon sequences are naturally associated with each other. In addition, the expressed antisense intron sequences are less than 350 bp in length.

Reviews on how enzymatic activity can be affected by expression of particular nucleotide sequences may be found in the teachings of Finnegan and McElroy [1994] Biotechnology 12 883-888; and Matzke and Matzke [1995] TIG 11 1-3.

Whilst it is known that enzymatic activity can be affected by expression of particular nucleotide sequences there is still a need for a method that can more reliably and/or more efficiently and/or more specifically affect enzymatic activity.

According to a first aspect of the present invention there is provided a method of affecting enzymatic activity in a plant (or a cell, a tissue or an organ thereof) comprising expressing in the plant (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence partially or completely codes for (is) an intron of the potato class A SBE gene in an antisense orientation optionally together with a nucleotide sequence which codes, partially or completely, for an intron of a class B starch branching enzyme in an antisense or sense orientation; and wherein the nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.

According to a second aspect of the present invention there is provided a method of affecting enzymatic activity in a starch producing organism (or a cell, a tissue or an

organ thereof) comprising expressing in the starch producing organism (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence codes, partially or completely, for an intron of the potato class A SBE gene, in an antisense orientation optionally together with a nucleotide sequence which codes, partially or completely, for an intron of a class B starch branching enzyme in an antisense or sense orientation; and wherein starch branching enzyme activity is affected and/or the levels of amylopectin are affected and/or the composition of starch is changed.

Preferably, the class A SBE gene antisense intron construct is used in combination with a potato class B SBE gene antisense intron construct as defined in PCT/EP96/03052. However, it may also be used independently thereof, to target class A SBE alone, or in combination with other transgenes, to further manipulate starch quality in potato plants.

According to a third aspect of the present invention, therefore, there is provided an antisense sequence comprising the nucleotide sequence shown as any one of SEQ.I.D. No. 15 to SEQ.I.D. No. 27 and the complement of SEQ. ID. No.38, or a variant, derivative or homologue thereof.

According to a fourth aspect of the present invention there is provided a promoter comprising the sequence shown as SEQ.I.D. No. 14 or a variant, derivative or homologue thereof.

According to a fifth aspect of the present invention there is provided a construct capable of comprising or expressing the present invention.

According to a sixth aspect of the present invention there is provided a vector comprising or expressing the present invention.

According to a seventh aspect of the present invention there is provided a cell, tissue or organ comprising or expressing the present invention.

According to an eighth aspect of the present invention there is provided a transgenic starch producing organism comprising or expressing the present invention.

According to a ninth aspect of the present invention there is provided a starch obtained from the present invention.

According to a tenth aspect of the present invention there is provided pSS17 and pSS18.

According to an eleventh aspect of the present invention there is provided a nucleotide sequence that is antisense to any one or more of the intron sequences obtainable from class A SBE, and especially those obtainable from intron 1 of class A SBE as set forth in SEQ. ID. No. 38.

5 A key advantage of the present invention is that it provides a method for preparing modified starches that is not dependent on the need for post-harvest modification of starches. Thus the method of the present invention obviates the need for the use of hazardous chemicals that are normally used in the post-harvest modification of starches.

In addition, the present invention provides *inter alia* genetically modified plants
10 which are capable of producing modified and/or novel and/or improved starches whose properties would satisfy various industrial requirements.

Thus, the present invention provides a method of preparing tailor-made starches in plants which could replace the post-harvest modified starches.

Also, the present invention provides a method that enables modified starches to be
15 prepared by a method that can have a more beneficial effect on the environment than the known post-harvest modification methods which are dependent on the use of hazardous chemicals and large quantities of energy.

An other key advantage of the present invention is that it provides a method that may more reliably and/or more efficiently and/or more specifically affect enzymatic
20 activity when compared to the known methods of affecting enzymatic activity. With regard to this advantage of the present invention it is to be noted that there is some degree of homology between coding regions of SBEs. However, there is little or no homology with the intron sequences of SBEs.

Thus, antisense intron expression provides a mechanism to affect selectively the
25 expression of a particular class A SBE. This advantageous aspect could be used, for example, to reduce or eliminate a particular SBE enzyme, especially a class A SBE enzyme, and replace that enzyme with another enzyme which can be another branching enzyme or even a recombinant version of the affected enzyme or even a hybrid enzyme which could for example comprise part of a SBE enzyme from one source and at least a
30 part of another SBE enzyme from another source. This particular feature of the present

invention is covered by the combination aspect of the present invention which is discussed in more detail later.

Thus the present invention provides a mechanism for selectively affecting class A SBE activity. This is in contrast to the prior art methods which are dependent on the use of for example antisense exon expression whereby it would not be possible to introduce new SBE activity without affecting that activity as well.

In the context of the present invention, class B SBE is synonymous with SBE I: class A SBE is synonymous with SBE II. Class A SBE is as defined in WO96/34968, incorporated herein by reference. Preferably, the antisense intron construct used comprises intron 1 of class A SBE, which is 2.0 kb in length and is located starting at residue 45 of the coding sequence of class A SBE. The boundaries of the intron may be calculated by searching for consensus intron boundary sequences. and are shown in attached figure 13. Class B SBE is substantially as defined in the sequences given herein and in PCT/EP96/03052.

Preferably with the first aspect of the present invention starch branching enzyme activity is affected and/or the levels of amylopectin are affected and/or the composition of starch is changed.

Preferably with the second aspect of the present invention the nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.

Preferably with the fourth aspect of the present invention the promoter is in combination with a gene of interest ("GOI").

Preferably the enzymatic activity is reduced or eliminated.

Preferably the nucleotide sequence codes for at least substantially all of at least one intron in an antisense orientation.

Preferably the nucleotide sequence codes, partially or completely, for two or more introns and wherein each intron is in an anti-sense orientation.

Preferably the nucleotide sequence comprises at least 350 nucleotides (e.g. at least 350 bp), more preferably at least 500 nucleotides (e.g. at least 500 bp).

Preferably the nucleotide sequence comprises the complement of the sequence shown in SEQ. ID. No. 38, or a fragment thereof.

Preferably the nucleotide sequence is expressed by a promoter having a sequence shown as SEQ. I.D. No 14 or a variant, derivative or homologue thereof.

Preferably the transgenic starch producing organism is a plant.

A preferred aspect of the present invention therefore relates to a method of
5 affecting enzymatic activity in a plant (or a cell, a tissue or an organ thereof) comprising
expressing in the plant (or a cell, a tissue or an organ thereof) a nucleotide sequence
wherein the nucleotide sequence codes, partially or completely, for an intron in an
antisense orientation; wherein the nucleotide sequence does not contain a sequence that is
antisense to an exon sequence normally associated with the intron; and wherein starch
10 branching enzyme activity is affected and/or the levels of amylopectin are affected and/or
the composition of starch is changed.

A more preferred aspect of the present invention therefore relates to a method of
affecting enzymatic activity in a plant (or a cell, a tissue or an organ thereof) comprising
expressing in the plant (or a cell, a tissue or an organ thereof) a nucleotide sequence
15 wherein the nucleotide sequence codes, partially or completely, for an intron in an
antisense orientation; wherein the nucleotide sequence does not contain a sequence that is
antisense to an exon sequence normally associated with the intron; wherein starch
branching enzyme activity is affected and/or the levels of amylopectin are affected and/or
the composition of starch is changed; and wherein the nucleotide sequence comprises the
20 sequence shown as any one of SEQ.I.D. No. 15 to SEQ.I.D. No. 27 or a variant,
derivative or homologue thereof, including combinations thereof.

The term "nucleotide" in relation to the present invention includes DNA and
RNA. Preferably it means DNA, more preferably DNA prepared by use of recombinant
DNA techniques.

25 The term "intron" is used in its normal sense as meaning a segment of
nucleotides, usually DNA, that is transcribed but does not encode part or all of an
expressed protein or enzyme.

The term "exon" is used in its normal sense as meaning a segment of nucleotides,
usually DNA, encoding part or all of an expressed protein or enzyme.

30 Thus, the term "intron" refers to gene regions that are transcribed into RNA
molecules, but which are spliced out of the RNA before the RNA is translated into a

protein. In contrast, the term "exon" refers to gene regions that are transcribed into RNA and subsequently translated into proteins.

The terms "variant" or "homologue" or "fragment" in relation to the nucleotide sequence of the present invention include any substitution of, variation of, modification
5 of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the respective nucleotide sequence providing the resultant nucleotide sequence can affect enzyme activity in a plant, or cell or tissue thereof, preferably wherein the resultant nucleotide sequence has at least the same effect as the complement of the sequence shown as SEQ.I.D. No. 38. In particular, the term "homologue" covers homology with respect
10 to similarity of structure and/or similarity of function providing the resultant nucleotide sequence has the ability to affect enzymatic activity in accordance with the present invention. With respect to sequence homology (i.e. similarity), preferably there is more than 80% homology, more preferably at least 85% homology, more preferably at least 90% homology, even more preferably at least 95% homology, more preferably at least
15 98% homology. The above terms are also synonymous with allelic variations of the sequences.

Likewise, the terms "variant" or "homologue" or "fragment" in relation to the promoter of the present invention include any substitution of, variation of, modification
20 of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the respective promoter sequence providing the resultant promoter sequence allows expression of a GOI, preferably wherein the resultant promoter sequence has at least the same effect as SEQ.I.D. No. 14. In particular, the term "homologue" covers homology with respect to similarity of structure and/or similarity of function providing the resultant promoter sequence has the ability to allow for expression of a GOI, such as a nucleotide
25 sequence according to the present invention. With respect to sequence homology (i.e. similarity), preferably there is more than 80% homology, more preferably at least 85% homology, more preferably at least 90% homology, even more preferably at least 95% homology, more preferably at least 98% homology. The above terms are also synonymous with allelic variations of the sequences.

The term "antisense" means a nucleotide sequence that is complementary to, and can therefore hybridise with, any one or all of the intron sequences of the present invention, including partial sequences thereof.

With the present invention, the antisense intron can be complementary to an entire
5 intron of the gene to be inhibited. However, in some circumstances, partial antisense sequences may be used (i.e. sequences that are not or do not comprise the full complementary sequence) providing the partial sequences affect enzymatic activity. Suitable examples of partial sequences include sequences that are shorter than the full complement of SEQ. ID. No. 38 but which comprise nucleotides that are at least
10 antisense to the sense intron sequences adjacent the respective exon or exons.

With regard to the second aspect of the present invention (i.e. specifically affecting SBE activity), the nucleotide sequences of the present invention may comprise one or more sense or antisense exon sequences of the SBE gene, including complete or partial sequences thereof, providing the nucleotide sequences can affect SBE activity,
15 preferably wherein the nucleotide sequences reduce or eliminate SBE activity. Preferably, the nucleotide sequence of the second aspect of the present invention does not comprise an antisense exon sequence.

The term "vector" includes an expression vector and a transformation vector. The term "expression vector" means a construct capable of *in vivo* or *in vitro* expression. The
20 term "transformation vector" means a construct capable of being transferred from one species to another - such as from an *E. Coli* plasmid to a fungus or a plant cell, or from an *Agrobacterium* to a plant cell.

The term "construct" - which is synonymous with terms such as "conjugate", "cassette" and "hybrid" - in relation to the antisense nucleotide sequence aspect of the
25 present invention includes the nucleotide sequence according to the present invention directly or indirectly attached to a promoter. An example of an indirect attachment is the provision of a suitable spacer group such as an intron sequence, such as the *ShI*-intron or the ADH intron, intermediate the promoter and the nucleotide sequence of the present invention. The same is true for the term "fused" in relation to the present invention
30 which includes direct or indirect attachment. The terms do not cover the natural

combination of the wild type SBE gene when associated with the wild type SBE gene promoter in their natural environment.

The construct may even contain or express a marker which allows for the selection of the genetic construct in, for example, a plant cell into which it has been transferred. Various markers exist which may be used in, for example, plants - such as mannose. Other examples of markers include those that provide for antibiotic resistance - e.g. resistance to G418, hygromycin, bleomycin, kanamycin and gentamycin.

The construct of the present invention preferably comprises a promoter. The term "promoter" is used in the normal sense of the art, e.g. an RNA polymerase binding site in the Jacob-Monod theory of gene expression. Examples of suitable promoters are those that can direct efficient expression of the nucleotide sequence of the present invention and/or in a specific type of cell. Some examples of tissue specific promoters are disclosed in WO 92/11375.

The promoter could additionally include conserved regions such as a Pribnow Box or a TATA box. The promoters may even contain other sequences to affect (such as to maintain, enhance, decrease) the levels of expression of the nucleotide sequence of the present invention. Suitable examples of such sequences include the *Shl*-intron or an ADH intron. Other sequences include inducible elements - such as temperature, chemical, light or stress inducible elements. Also, suitable elements to enhance transcription or translation may be present. An example of the latter element is the TMV 5' leader sequence (see Sleat Gene 217 [1987] 217-225; and Dawson Plant Mol. Biol. 23 [1993] 97).

As mentioned, the construct and/or the vector of the present invention may include a transcriptional initiation region which may provide for regulated or constitutive expression. Any suitable promoter may be used for the transcriptional initiation region, such as a tissue specific promoter. In one aspect, preferably the promoter is the patatin promoter or the E35S promoter. In another aspect, preferably the promoter is the SBE promoter.

If, for example, the organism is a plant then the promoter can be one that affects expression of the nucleotide sequence in any one or more of seed, tuber, stem, sprout, root and leaf tissues, preferably tuber. By way of example, the promoter for the

nucleotide sequence of the present invention can be the α -Amy 1 promoter (otherwise known as the Amy 1 promoter, the Amy 637 promoter or the α -Amy 637 promoter) as described in our co-pending UK patent application No. 9421292.5 filed 21 October 1994. Alternatively, the promoter for the nucleotide sequence of the present invention can be the
5 α -Amy 3 promoter (otherwise known as the Amy 3 promoter, the Amy 351 promoter or the α -Amy 351 promoter) as described in our co-pending UK patent application No. 9421286.7 filed 21 October 1994.

The present invention also encompasses the use of a promoter to express a nucleotide sequence according to the present invention, wherein a part of the promoter is
10 inactivated but wherein the promoter can still function as a promoter. Partial inactivation of a promoter in some instances is advantageous. In particular, with the Amy 351 promoter mentioned earlier it is possible to inactivate a part of it so that the partially inactivated promoter expresses the nucleotide sequence of the present invention in a more specific manner such as in just one specific tissue type or organ. The term "inactivated"
15 means partial inactivation in the sense that the expression pattern of the promoter is modified but wherein the partially inactivated promoter still functions as a promoter. However, as mentioned above, the modified promoter is capable of expressing a gene coding for the enzyme of the present invention in at least one (but not all) specific tissue of the original promoter. Examples of partial inactivation include altering the folding
20 pattern of the promoter sequence, or binding species to parts of the nucleotide sequence, so that a part of the nucleotide sequence is not recognised by, for example, RNA polymerase. Another, and preferable, way of partially inactivating the promoter is to truncate it to form fragments thereof. Another way would be to mutate at least a part of the sequence so that the RNA polymerase can not bind to that part or another part.
25 Another modification is to mutate the binding sites for regulatory proteins for example the CreA protein known from filamentous fungi to exert carbon catabolite repression, and thus abolish the catabolite repression of the native promoter.

The construct and/or the vector of the present invention may include a transcriptional termination region.

30 The nucleotide according to the present invention can be expressed in combination (but not necessarily at the same time) with an additional construct. Thus the present

invention also provides a combination of constructs comprising a first construct comprising the nucleotide sequence according to the present invention operatively linked to a first promoter; and a second construct comprising a GOI operatively linked to a second promoter (which need not be the same as the first promoter). With this aspect of
5 the present invention the combination of constructs may be present in the same vector, plasmid, cells, tissue, organ or organism. This aspect of the present invention also covers methods of expressing the same, preferably in specific cells or tissues, such as expression in just a specific cell or tissue, of an organism, typically a plant. With this aspect of the present invention the second construct does not cover the natural combination of the gene
10 coding for an enzyme ordinarily associated with the wild type gene promoter when they are both in their natural environment.

An example of a suitable combination would be a first construct comprising the nucleotide sequence of the present invention and a promoter, such as the promoter of the present
15 invention, and a second construct comprising a promoter, such as the promoter of the present invention, and a GOI wherein the GOI codes for another starch branching enzyme either in sense or antisense orientation.

The above comments relating to the term "construct" for the antisense nucleotide aspect of the present invention are equally applicable to the term "construct" for the
20 promoter aspect of the present invention. In this regard, the term includes the promoter according to the present invention directly or indirectly attached to a GOI.

The term "GOI" with reference to the promoter aspect of the present invention or the combination aspect of the present invention means any gene of interest, which need not necessarily code for a protein or an enzyme - as is explained later. A GOI can be any
25 nucleotide sequence that is either foreign or natural to the organism in question, for example a plant.

Typical examples of a GOI include genes encoding for other proteins or enzymes that modify metabolic and catabolic processes. The GOI may code for an agent for introducing or increasing pathogen resistance.

The GOI may even be an antisense construct for modifying the expression of natural transcripts present in the relevant tissues. An example of such a GOI is the nucleotide sequence according to the present invention.

The GOI may even code for a protein that is non-natural to the host organism - e.g. a plant. The GOI may code for a compound that is of benefit to animals or humans. For example, the GOI could code for a pharmaceutically active protein or enzyme such as any one of the therapeutic compounds insulin, interferon, human serum albumin, human growth factor and blood clotting factors. The GOI may even code for a protein giving additional nutritional value to a food or feed or crop. Typical examples include plant proteins that can inhibit the formation of anti-nutritive factors and plant proteins that have a more desirable amino acid composition (e.g. a higher lysine content than a non-transgenic plant). The GOI may even code for an enzyme that can be used in food processing such as xylanases and α -galactosidase. The GOI can be a gene encoding for any one of a pest toxin, an antisense transcript such as that for α -amylase, a protease or a glucanase. Alternatively, the GOI can be a nucleotide sequence according to the present invention.

The GOI can be the nucleotide sequence coding for the arabinofuranosidase enzyme which is the subject of our co-pending UK patent application 9505479.7. The GOI can be the nucleotide sequence coding for the glucanase enzyme which is the subject of our co-pending UK patent application 9505475.5. The GOI can be the nucleotide sequence coding for the α -amylase enzyme which is the subject of our co-pending UK patent application 9413439.2. The GOI can be the nucleotide sequence coding for the α -amylase enzyme which is the subject of our co-pending UK patent application 9421290.9. The GOI can be any of the nucleotide sequences coding for the α -glucan lyase enzyme which are described in our co-pending PCT patent application PCT/EP94/03397.

In one aspect the GOI can even be a nucleotide sequence according to the present invention but when operatively linked to a different promoter.

The GOI could include a sequence that codes for one or more of a xylanase, an arabinase, an acetyl esterase, a rhamnogalacturonase, a glucanase, a pectinase, a branching enzyme or another carbohydrate modifying enzyme or proteinase. Alternatively, the GOI may be a sequence that is antisense to any of those sequences.

As mentioned above, the present invention provides a mechanism for selectively affecting a particular enzymatic activity. In an important application of the present invention it is now possible to reduce or eliminate expression of a genomic nucleotide sequence coding for a genomic protein or enzyme by expressing an antisense intron construct for that particular genomic protein or enzyme and (e.g. at the same time) expressing a recombinant version of that enzyme or protein - in other words the GOI is a recombinant nucleotide sequence coding for the genomic enzyme or protein. This application allows expression of desired recombinant enzymes and proteins in the absence of (or reduced levels of) respective genomic enzymes and proteins. Thus the desired recombinant enzymes and proteins can be easily separated and purified from the host organism. This particular aspect of the present invention is very advantageous over the prior art methods which, for example, rely on the use of anti-sense exon expression which methods also affect expression of the recombinant enzyme.

Thus, a further aspect of the present invention relates to a method of expressing a recombinant protein or enzyme in a host organism comprising expressing a nucleotide sequence coding for the recombinant protein or enzyme; and expressing a further nucleotide sequence wherein the further nucleotide sequence codes, partially or completely, for an intron in an antisense orientation; wherein the intron is an intron normally associated with the genomic gene encoding a protein or an enzyme corresponding to the recombinant protein or enzyme; and wherein the further nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron. Additional aspects cover the combination of those nucleotide sequences including their incorporation in constructs, vectors, cells, tissues and transgenic organisms.

Therefore the present invention also relates to a combination of nucleotide sequences comprising a first nucleotide sequence coding for a recombinant enzyme; and a second nucleotide sequence which corresponds to an intron in antisense orientation; wherein the intron is an intron that is associated with a genomic gene encoding an enzyme corresponding to the recombinant enzyme; and wherein the second nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.

The GOI may even code for one or more introns, such as any one or more of the intron sequences presented in the attached sequence listings. For example, the present invention also covers the expression of for example an antisense intron (e.g. the complement of SEQ. ID. No. 38) in combination with for example a sense intron which
5 preferably is not complementary to the antisense intron sequence (e.g. SEQ.I.D.No. 2 or another class A SBE intron).

The terms "cell", "tissue" and "organ" include cell, tissue and organ *per se* and when within an organism.

The term "organism" in relation to the present invention includes any organism
10 that could comprise the nucleotide sequence according to the present invention and/or wherein the nucleotide sequence according to the present invention can be expressed when present in the organism. Preferably the organism is a starch producing organism such as any one of a plant, algae, fungi, yeast and bacteria, as well as cell lines thereof. Preferably the organism is a plant.

15 The term "starch producing organism" includes any organism that can biosynthesise starch. Preferably, the starch producing organism is a plant.

The term "plant" as used herein includes any suitable angiosperm, gymnosperm, monocotyledon and dicotyledon. Typical examples of suitable plants include vegetables such as potatoes; cereals such as wheat, maize, and barley; fruit; trees; flowers; and other
20 plant crops. Preferably, the term means "potato".

The term "transgenic organism" in relation to the present invention includes any organism that comprises the nucleotide sequence according to the present invention and/or products obtained therefrom, and/or wherein the nucleotide sequence according to the present invention can be expressed within the organism. Preferably the nucleotide
25 sequence of the present invention is incorporated in the genome of the organism. Preferably the transgenic organism is a plant, more preferably a potato.

To prepare the host organism one can use prokaryotic or eukaryotic organisms. Examples of suitable prokaryotic hosts include *E. coli* and *Bacillus subtilis*. Teachings on the transformation of prokaryotic hosts is well documented in the art, for example see
30 Sambrook *et al* (Sambrook *et al.* in Molecular Cloning: A Laboratory Manual, 2nd edition. 1989, Cold Spring Harbor Laboratory Press).

Even though the enzyme according to the present invention and the nucleotide sequence coding for same are not disclosed in EP-B-0470145 and CA-A-2006454, those two documents do provide some useful background commentary on the types of techniques that may be employed to prepare transgenic plants according to the present invention. Some of these background teachings are now included in the following commentary.

The basic principle in the construction of genetically modified plants is to insert genetic information in the plant genome so as to obtain a stable maintenance of the inserted genetic material.

Several techniques exist for inserting the genetic information, the two main principles being direct introduction of the genetic information and introduction of the genetic information by use of a vector system. A review of the general techniques may be found in articles by Potrykus (Annu Rev Plant Physiol Plant Mol Biol [1991] 42:205-225) and Christou (Agro-Food-Industry Hi-Tech March/April 1994 17-27).

Thus, in one aspect, the present invention relates to a vector system which carries a nucleotide sequence or construct according to the present invention and which is capable of introducing the nucleotide sequence or construct into the genome of an organism, such as a plant.

The vector system may comprise one vector, but it can comprise two vectors. In the case of two vectors, the vector system is normally referred to as a binary vector system. Binary vector systems are described in further detail in Gynheung An *et al.* (1980), Binary Vectors, *Plant Molecular Biology Manual A3*, 1-19.

One extensively employed system for transformation of plant cells with a given promoter or nucleotide sequence or construct is based on the use of a Ti plasmid from *Agrobacterium tumefaciens* or a Ri plasmid from *Agrobacterium rhizogenes* An *et al.* (1986), *Plant Physiol.* 81, 301-305 and Butcher D.N. *et al.* (1980), *Tissue Culture Methods for Plant Pathologists*, eds.: D.S. Ingrams and J.P. Helgeson, 203-208. Several different Ti and Ri plasmids have been constructed which are suitable for the construction of the plant or plant cell constructs described above. A non-limiting example of such a Ti plasmid is pGV3850.

The nucleotide sequence or construct of the present invention should preferably be inserted into the Ti-plasmid between the terminal sequences of the T-DNA or adjacent a T-DNA sequence so as to avoid disruption of the sequences immediately surrounding the T-DNA borders, as at least one of these regions appears to be essential for insertion of modified T-DNA into the plant genome.

As will be understood from the above explanation, if the organism is a plant the vector system of the present invention is preferably one which contains the sequences necessary to infect the plant (e.g. the *vir* region) and at least one border part of a T-DNA sequence, the border part being located on the same vector as the genetic construct.

Furthermore, the vector system is preferably an *Agrobacterium tumefaciens* Ti-plasmid or an *Agrobacterium rhizogenes* Ri-plasmid or a derivative thereof. As these plasmids are well-known and widely employed in the construction of transgenic plants, many vector systems exist which are based on these plasmids or derivatives thereof.

In the construction of a transgenic plant the nucleotide sequence or construct of the present invention may be first constructed in a microorganism in which the vector can replicate and which is easy to manipulate before insertion into the plant. An example of a useful microorganism is *E. coli*, but other microorganisms having the above properties may be used. When a vector of a vector system as defined above has been constructed in *E. coli*, it is transferred, if necessary, into a suitable *Agrobacterium* strain, e.g. *Agrobacterium tumefaciens*. The Ti-plasmid harbouring the nucleotide sequence or construct of the present invention is thus preferably transferred into a suitable *Agrobacterium* strain, e.g. *A. tumefaciens*, so as to obtain an *Agrobacterium* cell harbouring the promoter or nucleotide sequence or construct of the present invention, which DNA is subsequently transferred into the plant cell to be modified.

If, for example, for the transformation the Ti- or Ri-plasmid of the plant cells is used, at least the right boundary and often however the right and the left boundary of the Ti- and Ri-plasmid T-DNA, as flanking areas of the introduced genes, can be connected. The use of T-DNA for the transformation of plant cells has been intensively studied and is described in EP-A-120516; Hoekema, in: The Binary Plant Vector System Offset-drukkerij Kanters B.B., Alblasterdam, 1985, Chapter V; Fraley, *et al.*, Crit. Rev. Plant Sci., 4:1-46; and An *et al.*, EMBO J. (1985) 4:277-284.

Direct infection of plant tissues by *Agrobacterium* is a simple technique which has been widely employed and which is described in Butcher D.N. *et al.* (1980), *Tissue Culture Methods for Plant Pathologists*, eds.: D.S. Ingrams and J.P. Helgeson, 203-208. For further teachings on this topic see Potrykus (Annu Rev Plant Physiol Plant Mol Biol
5 [1991] 42:205-225) and Christou (Agro-Food-Industry Hi-Tech March/April 1994 17-27). With this technique, infection of a plant may be performed in or on a certain part or tissue of the plant, i.e. on a part of a leaf, a root, a stem or another part of the plant.

Typically, with direct infection of plant tissues by *Agrobacterium* carrying the GOI (such as the nucleotide sequence according to the present invention) and, optionally,
10 a promoter, a plant to be infected is wounded, e.g. by cutting the plant with a razor blade or puncturing the plant with a needle or rubbing the plant with an abrasive. The wound is then inoculated with the *Agrobacterium*. The inoculated plant or plant part is then grown on a suitable culture medium and allowed to develop into mature plants.

When plant cells are constructed, these cells may be grown and maintained in
15 accordance with well-known tissue culturing methods such as by culturing the cells in a suitable culture medium supplied with the necessary growth factors such as amino acids, plant hormones, vitamins, etc.

Regeneration of the transformed cells into genetically modified plants may be accomplished using known methods for the regeneration of plants from cell or tissue
20 cultures, for example by selecting transformed shoots using an antibiotic and by subculturing the shoots on a medium containing the appropriate nutrients, plant hormones, etc.

Further teachings on plant transformation may be found in EP-A-0449375.

As reported in CA-A-2006454, a large amount of cloning vectors are available
25 which contain a replication system in *E. coli* and a marker which allows a selection of the transformed cells. The vectors contain for example pBR 322, pUC series, M13 mp series, pACYC 184 etc. In this way, the nucleotide or construct of the present invention can be introduced into a suitable restriction position in the vector. The contained plasmid is then used for the transformation in *E.coli*. The *E.coli* cells are cultivated in a suitable
30 nutrient medium and then harvested and lysed. The plasmid is then recovered. As a method of analysis there is generally used sequence analysis, restriction analysis,

electrophoresis and further biochemical-molecular biological methods. After each manipulation, the used DNA sequence can be restricted and connected with the next DNA sequence. Each sequence can be cloned in the same or different plasmid.

After the introduction of the nucleotide sequence or construct according to the present invention in the plants the presence and/or insertion of further DNA sequences may be necessary - such as to create combination systems as outlined above (e.g. an organism comprising a combination of constructs).

The above commentary for the transformation of prokaryotic organisms and plants with the nucleotide sequence of the present invention is equally applicable for the transformation of those organisms with the promoter of the present invention.

In summation, the present invention relates to affecting enzyme activity by expressing antisense intron sequences.

Also, the present invention relates to a promoter useful for the expression of those antisense intron sequences.

The following samples have been deposited in accordance with the Budapest Treaty at the recognised depositary The National Collections of Industrial and Marine Bacteria Limited (NCIMB) at 23 St Machar Drive, Aberdeen, Scotland, AB2 1RY, United Kingdom, on 13 July 1995:

NCIMB 40753 (which refers to pBEA 8 as described herein);
NCIMB 40751 (which refers to λ -SBE 3.2 as described herein), and
NCIMB 40752 (which refers to λ -SBE 3.4 as described herein).

The following sample has been deposited in accordance with the Budapest Treaty at the recognised depositary The National Collections of Industrial and Marine Bacteria Limited (NCIMB) at 23 St Machar Drive, Aberdeen, Scotland, AB2 1RY, United Kingdom, on 9 July 1996:

NCIMB 40815 (which refers to pBEA 9 as described herein).

A highly preferred embodiment of the present invention therefore relates to a method of affecting enzymatic activity in a plant (or a cell, a tissue or an organ thereof) comprising expressing in the plant (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence codes, partially or completely, for an intron in an antisense orientation; wherein the nucleotide sequence does not contain a sequence that

is antisense to an exon sequence normally associated with the intron; wherein starch branching enzyme activity is affected and/or the levels of amylopectin are affected and/or the composition of starch is changed; and wherein the nucleotide sequence is antisense to intron 1 of class A SBE as set forth in SEQ. ID. No. 38, or any other intron of class A SBE, including fragments thereof, and including combinations of class A antisense intron sequences and class B antisense intron sequences. The sequence of introns of class A SBE other than intron 1 may be obtained by sequencing of, for example, potato class A SBE genomic DNA, isolatable by hybridisation screening of a genomic DNA library with class A SBE cDNA obtainable according to WO96/34968 according to methods well known in the art and set forth, for example, in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, 1989.

The present invention will now be described only by way of example, in which reference is made to the following attached Figures:

Figure 1, which is a schematic representation of the biosynthesis of amylose and amylopectin;

Figure 2, which is a diagrammatic representation of the α -1-4-links and the α -1-6 links of amylopectin;

Figure 3, which is a diagrammatic representation of a possible antisense-RNA inhibition mechanism;

Figure 4, which is a diagrammatic representation of the exon-intron structure of a genomic SBE clone;

Figure 5, which is a plasmid map of pPATA1, which is 3936 bp in size;

Figure 6, which is a plasmid map of pABE6, which is 5106 bp in size;

Figure 7, which is a plasmid map of pVictorIV Man, which is 7080 bp in size;

Figure 8, which is a plasmid map of pBEA8, which is 9.54 kb in size;

Figure 9, which is a plasmid map of pBEA9, which is 9.54 kb in size;

Figure 10, which is a plasmid map of pBEP2, which is 10.32 kb in size;

Figure 11, which is a plasmid map of pVictor5a, which is 9.12 kb in size;

Figure 12, which shows the full genomic nucleotide sequence for SBE including the promoter, exons and introns;

Figure 13, which shows the positioning of intron 1 in the class A and class B SBE genes;

Figure 14, which shows the sequence of intron 1 of the potato class A SBE;

Figure 15, which shows the structure of pSS17; and

5 Figure 16, which shows the structure of pSS18.

Figures 1 and 2 were referred to above in the introductory description concerning starch in general. Figure 3 was referred to above in the introductory description concerning antisense expression.

As mentioned, Figure 4 is a diagrammatic representation of the exon-intron
10 structure of a genomic SBE clone, the sequence of which is shown in Figure 12. This clone, which has about 11.5 k base pairs, comprises 14 exons and 13 introns. The introns are numbered in increasing order from the 5' end to the 3' end and correspond to SEQ.I.D.No.s 1-13, respectively. Their respective antisense intron sequences are shown as SEQ.I.D.No.s 15-27.

15 In more detail, Figures 4 and 12 present information on the 11478 base pairs of a potato SBE gene. The 5' region from nucleotides 1 to 2082 contain the promoter region of the SBE gene. A TATA box candidate at nucleotide 2048 to 2051 is boxed. The homology between a potato SBE cDNA clone (Poulsen & Kreiberg (1993) Plant Physiol 102: 1053-1054) and the exon DNAs begin at 2083 bp and end at 9666 bp.

20 The homology between the cDNA and the exon DNA is indicated by nucleotides in upper case letters, while the translated amino acid sequences are shown in the single letter code below the exon DNA. Intron sequences are indicated by lower case letters.

Figures 5 to 7 are discussed below. As mentioned, Figure 8 is a plasmid map of pBEA8, which is 9.54 k base pairs in size; and Figure 9 is a plasmid map of pBEA9,
25 which is 9.54 k base pairs in size. Each of pBEA 8 and pBEA 9 comprises an antisense sequence to the first intron sequence of the potato SBE gene. This first intron sequence, which has 1177 base pairs, is shown in Figure 4 and lies between the first exon and the second exon.

30 These experiments and aspects of the present invention are now discussed in more detail.

EXPERIMENTAL PROTOCOL**ISOLATION, SUBCLONING IN PLASMIDS, AND SEQUENCING OF GENOMIC CLASS B SBE CLONES**

5 Various clones containing the potato class B SBE gene are isolated from a Desiree potato genomic library (Clontech Laboratories Inc., Palo Alto CA, USA) using radioactively labelled potato SBE cDNA (Poulsen & Kreiberg (1993) Plant Physiol. 102:1053-1054) as probe. The fragments of the isolated λ -phages containing SBE DNA (λ SBE 3.2 - NCIMB 40751 - and λ SBE-3.4 - NCIMB 40752) are identified by Southern
 10 analysis and then subcloned into pBluescript II vectors (Clontech Laboratories Inc., Palo Alto CA, USA). λ SBE 3.2 contains a 15 kb potato DNA insert and λ SBE-3.4 contains a 13 kb potato DNA insert. The resultant plasmids are called pGB3, pGB11, pGB15, pGB16 and pGB25 (see discussion below). The respective inserts are then sequenced using the Pharmacia Autoread Sequencing Kit (Pharmacia. Uppsala) and a A.L.F. DNA
 15 sequencer (Pharmacia, Uppsala).

In total, a stretch of 11.5 kb of the class B SBE gene is sequenced. The sequence is deduced from the above-mentioned plasmids, wherein: pGB25 contains the sequences from 1 bp to 836 bp, pGB15 contains the sequences from 735 bp to 2580 bp, pGB16 contains the sequences from 2580 bp to 5093 bp, pGB11 contains the sequences from
 20 3348 bp to 7975 bp, and pGB3 contains the sequences from 7533 bp to 11468 bp.

In more detail, pGB3 is constructed by insertion of a 4 kb *EcoRI* fragment isolated from λ SBE 3.2 into the *EcoRI* site of pBluescript II SK (+). pGB11 is constructed by insertion of a 4.7 kb *XhoI* fragment isolated from λ SBE 3.4 into the *XhoI* site of pBluescript II SK (+). pGB15 is constructed by insertion of a 1.7 kb *SpeI* fragment
 25 isolated from λ SBE 3.4 into the *SpeI* site of pBluescript II SK (+). pGB16 is constructed by insertion of a 2.5 kb *SpeI* fragment isolated from λ SBE 3.4 into the *SpeI* site of pBluescript II SK (+). For the construction of pGB25 a PCR fragment is produced with the primers

5' GGA ATT CCA GTC GCA GTC TAC ATT AC 3'

30

(SEQ. ID. No.30)

and

5' CGG GAT CCA GAG GCA TTA AGA TTT CTG G 3'

(SEQ. ID. No. 31)

and λ SBE 3.4 as a template.

The PCR fragment is digested with *Bam*HI and *Eco*RI, and inserted in pBluescript
5 II SK (+) digested with the same restriction enzymes.

A class A SBE clone is derived similarly.

CONSTRUCTION OF CLASS B SBE ANTISENSE INTRON PLASMIDS pBEA8 and pBEA9

10 The SBE intron 1 is amplified by PCR using the oligonucleotides:

5' CGG GAT CCA AAG AAA TTC TCG AGG TTA CAT GG 3'

(SEQ. ID. No. 32)

and

5' CGG GAT CCG GGG TAA TTT TTA CTA ATT TCA TG 3'

15 (SEQ. ID. No. 33)

and the λ SBE 3.4 phage containing the SBE gene as template.

The PCR product is digested with *Bam*HI and inserted in an antisense orientation
in the *Bam*HI site of plasmid pPATA1 (described in WO 94/24292) between the patatin
promoter and the 35S terminator. This construction, pABE6, is digested with *Kpn*I, and
20 the 2.4 kb "patatin promoter-SBE intron 1- 35S terminator" *Kpn*I fragment is isolated and
inserted in the *Kpn*I site of the plant transformation vector pVictorIV Man. The *Kpn*I
fragment is inserted in two orientations yielding plasmids pBEA8 and pBEA9. pVictorIV
Man is shown in Figure 7 and is formed by insertion of a filled in *Xba*I fragment
containing a E35S promoter-manA-35S terminator cassette isolated from plasmid
25 pVictorIV SGiN Man (WO 94/24292) into the filled in *Xho*I site of pVictor IV. The
pVictor regions of pVictor IV Man contained between the co-ordinates 2.52 bp to 0.32 bp
(see Figure 7).

CONSTRUCTION OF CLASS A SBE ANTISENSE INTRON PLASMIDS pSS17 and pSS18

Construction of plasmid pSS17.

5 The 2122 bp intron 1 sequence of the potato SBEII gene is amplified by PCR from a genomic SBEII subclone using the primers 5' - CGG GAT CCC GTA TGT CTC ACT GTG TTT GTG GC - 3' (SEQ. ID. No. 34) and 5' - CGG GAT CCC CCT ACA TAC ATA TAT CAG ATT AG - 3' (SEQ. ID. No. 35). The PCR product is digested with BamHI and inserted in antisense orientation after a patatin promoter in the
10 BamHI site of a plant transformation vector in which the NPTII gene is used as selectable marker (see figure 15).

Construction of plasmid pSS18.

 The 2122 bp intron 1 sequence of the potato SBEII gene is amplified by PCR
15 from a genomic SBEII subclone using the primers 5' - CGG GAT CCC GTA TGT CTC ACT GTG TTT GTG GC - 3' (SEQ. ID. No. 34) and 5' - CGG GAT CCC CCT ACA TAC ATA TAT CAG ATT AG - 3' (SEQ. ID. No. 35). The PCR product is digested with BamHI and inserted in antisense orientation after a patatin promoter in the BamHI site of a plant transformation vector in which the *manA* gene is used as
20 selectable marker (see figure 16).

PRODUCTION OF TRANSGENIC POTATO PLANTS

Axenic stock cultures

 Shoot cultures of *Solanum tuberosum* 'Bintje' and 'Dianella' are maintained on a
25 substrate (LS) of a formula according to Linsmaier, E.U. and Skoog, F. (1965), *Physiol. Plant.* 18: 100-127, in addition containing 2 µM silver thiosulphate at 25°C and 16 h light/8 h dark.

 The cultures are subcultured after approximately 40 days. Leaves are then cut off the shoots and cut into nodal segments (approximately 0.8 cm) each containing one node.

Inoculation of potato tissues

Shoots from approximately 40 days old shoot cultures (height approximately 5-6 cms) are cut into internodal segments (approximately 0.8 cm). The segments are placed into liquid LS-substrate containing the transformed *Agrobacterium tumefaciens* containing the binary vector of interest. The *Agrobacterium* are grown overnight in YMB-substrate (di-potassium hydrogen phosphate, trihydrate (0.66 g/l); magnesium sulphate, heptahydrate (0.20 g/l); sodium chloride (0.10 g/l); mannitol (10.0 g/l); and yeast extract (0.40 g/l)) containing appropriate antibiotics (corresponding to the resistance gene of the *Agrobacterium* strain) to an optical density at 660 nm (OD-660) of approximately 0.8, centrifuged and resuspended in the LS-substrate to an OD-660 of 0.5.

The segments are left in the suspension of *Agrobacterium* for 30 minutes and then the excess of bacteria are removed by blotting the segments on sterile filter paper.

Co-cultivation

The shoot segments are co-cultured with bacteria for 48 hours directly on LS-substrate containing agar (8.0 g/l), 2,4-dichlorophenoxyacetic acid (2.0 mg/l) and trans-zeatin (0.5 mg/l). The substrate and also the explants are covered with sterile filter papers, and the petri dishes are placed at 25°C and 16 h light/ 8 dark.

"Washing" procedure

After the 48 h on the co-cultivation substrate the segments are transferred to containers containing liquid LS-substrate containing 800 mg/l carbenicillin. The containers are gently shaken and by this procedure the major part of the *Agrobacterium* is either washed off the segments and/or killed.

Selection

After the washing procedure the segments are transferred to plates containing the LS-substrate, agar (8 g/l), trans-zeatin (1-5 mg/l), gibberellic acid (0.1 mg/l), carbenicillin (800 mg/l), and kanamycin sulphate (50-100 mg/l) or phosphinotricin (1-5 mg/l) or mannose (5 g/l) depending on the vector construction used. The segments are sub-cultured to fresh substrate each 3-4 weeks.

In 3 to 4 weeks, shoots develop from the segments and the formation of new shoots continued for 3-4 months.

Rooting of regenerated shoots

- 5 The regenerated shoots are transferred to rooting substrate composed of LS-substrate, agar (8 g/l) and carbenicillin (800 mg/l).

 The transgenic genotype of the regenerated shoot is verified by testing the rooting ability on the above mentioned substrates containing kanamycin sulphate (200 mg/l), by performing NPTII assays (Radke, S. E. et al, Theor. Appl. Genet. (1988), 75: 685-694) or by performing PCR analysis according to Wang *et al* (1993, NAR 21 pp 4153-4154).
10 Plants which are not positive in any of these assays are discarded or used as controls. Alternatively, the transgenic plants could be verified by performing a GUS assay on the co-introduced β -glucuronidase gene according to Hodal, L. *et al.* (Pl. Sci. (1992), 87: 115-122).

15

Transfer to soil

- The newly rooted plants (height approx. 2-3 cms) are transplanted from rooting substrate to soil and placed in a growth chamber (21°C, 16 hour light 200-400uE/m²/sec). When the plants are well established they are transferred to the greenhouse, where they
20 are grown until tubers had developed and the upper part of the plants are senescing.

Harvesting

 The potatoes are harvested after about 3 months and then analysed.

25 **BRANCHING ENZYME ANALYSIS**

- The class A and class B SBE expression in the transgenic potato lines is measured using the SBE assays described by Blennow and Johansson (Phytochemistry (1991) 30:437-444) and by standard Western procedures using antibodies directed against potato SBE.

30

STARCH ANALYSIS

Starch is isolated from potato tubers and analysed for the amylose:amylopectin ratio (Hovenkamp-Hermelink et al. (1988) Potato Research 31:241-246). In addition, the chain length distribution of amylopectin is determined by analysis of isoamylase digested starch on a Dionex HPAEC.

The number of reducing ends in isoamylase digested starch is determined by the method described by N. Nelson (1944) J. Biol.Chem. 153:375-380.

The results reveal that there is a reduction in the level of synthesis of SBE and/or the level of activity of SBE and/or the composition of starch SBE in the transgenic plants.

CONSTRUCTION OF SBE PROMOTER CONSTRUCT

An SBE promoter fragment is amplified from λ -SBE 3.4 using primers:

5' CCA TCG ATA CTT TAA GTG ATT TGA TGG C 3'

(SEQ. ID. No. 36)

and

5' CGG GAT CCT GTT CTG ATT CTT GAT TTC C 3'.

(SEQ. ID. No. 37)

The PCR product is digested with *ClaI* and *BamHI*. The resultant 1.2 kb fragment is then inserted in pVictor5a (see Figure 11) linearised with *ClaI* and *BglII* yielding pBEP2 (see Figure 10).

STARCH BRANCHING ENZYME MEASUREMENTS OF POTATO TUBERS

Potatoes from potato plants transformed with pBEA8, pBEA9, pSS17 or pSS18 are cut in small pieces and homogenised in extraction buffer (50 mM Tris-HCl pH 7.5, Sodium-dithionite (0.1 g/l), and 2 mM DTT) using a Ultra-Turax homogenizer; 1 g of Dowex xl. is added pr. 10 g of tuber. The crude homogenate is filtered through a miracloth filter and centrifuged at 4°C for 10 minutes at 24.700 g. The supernatant is used for starch branching enzyme assays.

The starch branching enzyme assays are carried out at 25°C in a volume of 400 μ l composed of 0.1 M Na citrate buffer pH 7.0, 0.75 mg/ml amylose, 5 mg/ml bovine serum albumin and the potato extract. At 0, 15, 30 and 60 minutes aliquots of 50 μ l are

removed from the reaction into 20 µl 3 N HCl. 1 ml of iodine solution is added and the decrease in absorbance at 620 nm is measured with an ELISA spectrophotometer.

The starch branching enzyme (SBE) levels are measured in tuber extracts from 34 transgenic *Dianella* potato plants transformed with plasmid pBEA8, pSS17 and pSS18.

5 The transformed transgenic lines produce tubers which have SBE levels that are 10% to 15% of the appropriate class A or class B SBE levels found in non transformed *Dianella* plants.

In a further experiment, plasmids pSS17 and pBEA8 are cotransfected into potato plants, as described above. In the cotransfectants, when analysed as set forth above,
10 simultaneous reduction of class A and class B SBE levels are observed.

SUMMATION

The above-mentioned examples relate to the isolation, sequencing and utilisation of antisense intron constructs derived from a gene for potato class A and class B SBE.
15 These SBE intron antisense constructs can be introduced into plants, such as potato plants. After introduction, a reduction in the level of synthesis of SBE and/or the level of activity of SBE and/or the composition of starch in plants can be achieved.

Without wishing to be bound by theory it is believed that the expressed anti-sense nucleotide sequence of the present invention binds to sense introns on pre-mRNA and
20 thereby prevents pre-mRNA splicing and/or subsequent translation of mRNA. This binding therefore is believed to reduce the level of plant enzyme activity (in particular class A and class B SBE activity), which in turn for SBE activity is believed to influence the amylose:amylopectin ratio and thus the branching pattern of amylopectin.

Thus, the present invention provides a method wherein it is possible to manipulate
25 the starch composition in plants, or tissues or cells thereof, such as potato tubers, by reducing the level of SBE activity by using an antisense-RNA technique using antisense intron sequences.

The simultaneous reduction or elimination of class A and class B SBE sequences from the doubly transformed potato plants, moreover, offers the possibility to transform
30 such plants with different SBE genes at will, thus allowing the manipulation of branching in starch according to the desired result.

Other modifications of the present invention will be apparent to those skilled in the art without departing from the scope of the present invention.

The following pages present a number of sequence listings which have been consecutively numbered from SEQ.I.D. No. 1 - SEQ.I.D. No. 38. In brief, SEQ.I.D. No. 1 - SEQ.I.D. No. 13 represent sense intron sequences (genomic DNA); SEQ.I.D. No. 14 represents the SBE promoter sequence (genomic sequence); SEQ.I.D. No. 15 - SEQ.I.D. No. 27 represent antisense intron sequences; and SEQ. I.D. No. 28 represents is the sequence complementary to the SBE promoter sequence - i.e. the SBE promoter sequence in antisense orientation. The full genomic nucleotide sequence for class B SBE including the promoter, exons and introns is shown as SEQ. I.D. No. 29 and is explained by way of Figures 4 and 12 which highlight particular gene features. SEQ. ID. No. 30 to 37 show primers used in the methods set forth above. SEQ. ID. No. 38 shows the sequence of intron 1 of class A SBE.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

- (A) NAME: DANISCO A/S
(B) STREET: LANGEBOGADE 1
(C) CITY: COPENHAGEN K
(E) COUNTRY: DENMARK
(F) POSTAL CODE (ZIP): DK-1001

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(ii) TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION

15

(iii) NUMBER OF SEQUENCES: 38

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTAATTTTGA CTAATTTCAT GTTAATTTCA ATTATTTTGA GCCTTTGCAT TTCATTTTCC 60
45 AATATATCTG GATCATCTCC TTAGTTTTTT ATTTTATTTT TTATAATATC AAATATGGAA 120
GAAAAATGAC ACTTGTAGAG CCATATGTAA GTATCATGTG ACAAATTGTC AAGGTGGTTG 180
AGTGTATAAA ATTCAAAAAT TGAGAGATGG AGGGGGGGTG GGGGAAGACA ATATTTAGAA 240
50 AGAGTGTCTT AGGAGGTTAT GGAGGACACG GATGAGGGGT AGAAGGTTAG TTAGGTATTT 300
GAGTGTGTC TGGCTTATCC TTTCATACTA GTAGTCGTGG AATTATTTGG GTAGTTCTTT 360
55 GTTTTGTTAT TTGATCTTTG TTATTCTATT TTCTGTTTCT TGTACTTCGA TTATTGTATT 420
ATATATCTTG TCGTAGTTAT TGTTCCTCGG TAAGAATGCT CTAGCATGCT TCCTTTAGTG 480

TTTTATCATG CCTTCTTTAT ATTGCGGTTG CTTTGAAATG CTTTACTTT AGCCGAGGGT 540
 CTATTAGAAA CAATCTCTCT ATCTCGTAAG GTAGGGGTAA AGTCCTCACC ACACTCCACT 600
 5 TGTGGGATTA CATTGTGTTT GTTGTGTAA ATCAATTATG TATACATAAT AAGTGGATT 660
 TTTACAACAC AAATACATGG TCAAGGGCAA AGTTCTGAAC ACATAAAGGG TTCATTATAT 720
 10 GTCCAGGGAT ATGATAAAAA TTGTTTCTTT GTGAAAGTTA TATAAGATTT GTTATGGCTT 780
 TTGCTGGAAA CATAATAAGT TATAATGCTG AGATAGCTAC TGAAGTTTGT TTTTCTAGC 840
 CTTTTAAATG TACCAATAAT AGATTCCGTA TCGAACGAGT ATGTTTTGAT TACCTGGTCA 900
 15 TGATGTTTCT ATTTTTTACA TTTTTTGGT GTTGAAGTGC AATTGAAAAT GTTGTATCCT 960
 ATGAGACGGA TAGTTGAGAA TGTGTTCTTT GTATGGACCT TGAGAAGCTC AAACGCTACT 1020
 20 CCAATAATTT CTATGAATTC AAATTCAGTT TATGGCTACC AGTCAGTCCA GAAATTAGGA 1080
 TATGCTGCAT ATACTGTTC AATTATACTG TAAAATTCT TAAGTTCTCA AGATATCCAT 1140
 GTAACCTCGA GAATTCTTT GACAG 1165
 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
 35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

45 GTATGTTTGA TAATTATAT GGTGTCATGG ATAGTATATA AATAGTTGGA AAACCTTCTGG 60
 ACTGGTGCTC ATGGCATATT TGATCTGTGC ACCGTGTGGA GATGTCAAAC ATGTGTTACT 120
 TCGTTCCGCC AATTATAAT ACCTTAACCT GGGAAAGACA GCTCTTACT CCTGTGGGCA 180
 50 TTTGTTATTT GAATTACAAT CTTTATGAGC ATGGTGTGTT CACATTATCA ACTTCTTTCA 240
 TGTGGTATAT AACAGTTTTT AGCTCCGTTA ATACCTTCT TCTTTTGAT ATAAACTAAC 300
 55 TGTGGTGAT TGCTTGC 317

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTAACAGCCA AAAGTTGTGC TTTAGGCAGT TTGACCTTAT TTTGGAAGAT GAATTGTTTA	60
TACCTACTTT GACTTTGCTA GAGAATTTTG CATACCGGG AGTAAGTAGT GGCTCCATTT	120
AGGTGGCACC TGGCCATTTT TTTGATCTTT TAAAAAGCTG TTTGATTGGG TCTTCAAAAA	180
AGTAGACAAG GTTTTTGGAG AAGTGACACA CCCCCGGAGT GTCAGTGGCA AAGCAAAGAT	240
TTTCACTAAG GAGATTCAAA ATATAAAAAA AGTATAGACA TAAAGAAGCT GAGGGGATTC	300
AACATGTACT ATACAAGCAT CAAATATAGT CTAAAGCAA TTTTGTAGAA ATAAAGAAAG	360
TCTTCCTTCT GTTGCTTCAC AATTCCTTC TATTATCATG AGTTACTCTT TCTGTTCGAA	420
ATAGCTTCCT TAATATTAAA TTCATGATAC TTTGTTGAG ATTTAGCAGT TTTTCTTGT	480
GTAAACTGCT CTCTTTTTTT GCAG	504

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTAGGTCCTC GTCTACTACA AAATAGTAGT TTCCATCATC ATAACAGATT TTCCTATTAA	60
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AGCATGATGT TGCAGCATCA TTGGCTTCT TACATGTTCT AATTGCTATT AAGGTTATGC 120
TTCTAATTAA CTCATCCACA ATGCAG 146

5 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

25 GTTTTGTTAT TCATACCTTG AAGCTGAATT TTGAACACCA TCATCACAGG CATTCGATT 60
CATGTTCTTA CTAGTCTTGT TATGTAAGAC ATTTTGAAAT GCAAAAGTTA AAATAATTGT 120
GTCTTTACTA ATTTGGACTT GATCCCATAC TCTTCCCTT AACAAAATGA GTCAATTCTA 180
30 TAAGTGCTTG AGAACTTACT ACTTCAGCAA TTAAACAG 218

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50 GTATTTTAAA TTTATTTCTA CAACTAAATA ATTCTCAGAA CAATTGTTAG ATAGAATCCA 60
AATATATACG TCCTGAAAGT ATAAAAGTAC TTATTTTCGC CATGGGCCTT CAGAATATTG 120
55 GTAGCCGCTG AATATCATGA TAAGTTATTT ATCCAGTGAC ATTTTATGT TCACTCCTAT 180
TATGTCTGCT GGATACAG 198

(2) INFORMATION FOR SEQ ID NO: 7:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

20 GTTTGTCTGT TTCTATTGCA TTTAAGGTT CATATAGGTT AGCCACGGAA AATCTCACTC 60
 TTTGTGAGGT AACCAGGGTT CTGATGGATT ATTCAATTTT CTCGTTTATC ATTTGTTTAT 120
 25 TCTTTTCATG CATTGTGTTT CTTTTTCAAT ATCCCTCTTA TTTGGAGGTA ATTTTCTCA 180
 TCTATTCACT TTTAGCTTCT AACCACAG 208

(2) INFORMATION FOR SEQ ID NO: 8:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTATGTCTTA CATCTTTAGA TATTTTGTGA TAATTACAAT TAGTTTGGCT TACTTGAACA 60
 50 AGATTCATTC CTCAAAATGA CCTGAAGTGT TGAACATCAA AGGGGTTGAA ACATAGAGGA 120
 AAACAACATG ATGAATGTTT CCATTGTCTA GGGATTTCTA TTATGTTGCT GAGAACAAAT 180
 GTCATCTTAA AAAAAACATT GTTTACTTTT TTGTAGTATA GAAGATTACT GTATAGAGTT 240
 55 TGCAAGTGTG TCTGTTTTGG AGTAATTGTG AAATGTTTGA TGAACCTGTA CAG 293

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

20 GTTCAAGTAT TTTGAATCGC AGCTTGTTAA ATAATCTAGT AATTTTTAGA TTGCTTACTT 60
GGAAGTCTAC TTGGTTCTGG GGATGATAGC TCATTCATC TTGTTCTACT TATTTTCCAA 120
CCGAATTCT GATTTTGTG TCGAGATCCA AGTATTAGAT TCATTACAC TTATTACCGC 180
25 CTCATTCTA CCACTAAGGC CTGATGAGC AGCTTAAGTT GATTCTTTGA AGCTATAGTT 240
TCAGGCTACC AATCCACAGC CTGCTATATT TGTTGGATAC TTACCTTTTC TTTACAATGA 300
30 AGTGATACTA ATTGAAATGG TCTAAATCTG ATATCTATAT TTCTCCGTCT TTCCTCCCCC 360
TCATGATGAA ATGCAG 376

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTAAAATCAT CTAAAGTTGA AAGTGTGGG TTTATGAAGT GCTTTAATTC TATCCAAGGA 60
55 CAAGTAGAAA CCTTTTACC TTCCATTCT TGATGATGGA TTTCATATTA TTTAATCCAA 120
TAGCTGGTCA AATTCGGTAA TAGCTGTACT GATTAGTTAC TTCACCTTGC AG 172

(2) INFORMATION FOR SEQ ID NO: 11:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

20 GTATATATGT TTTACTTATC CATGAAATTA TTGCTCTGCT TGTTTTAAAT GTACTGAACA 60
AGTTTTATGG AGAAGTAACT GAAACAAATC ATTTTCACAT TGTCTAATTT AACTCTTTTT 120
25 TCTGATCCTC GCATGACGAA AACAG 145

(2) INFORMATION FOR SEQ ID NO: 12:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

45 GTAAGGATTT GCTTGAATAA CTTTGTATAA TAAGATAACA GATGTAGGGT ACAGTTCTCT 60
CACCAAAAAG AACTGTAATT GTCTCATCCA TCTTTAGTTG TATAAGATAT CCGACTGTCT 120
50 GAGTTCGGAA GTGTTTGAGC CTCCTGCCCT CCCCTGCGT TGTTTAGCTA ATTCAAAAAG 180
GAGAAAAC TG TTTATTGATG ATCTTTGTCT TCATGCTGAC ATACAATCTG TTCTCATGAC 240
AG 242

55

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 797 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
10

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15 GTACAGTTCT TGCCGTGTGA CCTCCCTTTT TATTGTGGTT TTGTTCATAG TTATTTGAAT 60
20 GCGATAGAAG TTAAC TATTG ATTACCGCCA CAATCGCCAG TTAAGTCCTC TGAAC TACTA 120
 ATTTGAAAGG TAGGAATAGC CGTAATAAGG TCTACTTTTG GCATCTTACT GTTACAAAAC 180
25 AAAAGGATGC CAAAAAATT CTTCTCTATC CTCTTTTCC CTAAACCAGT GCATGTAGCT 240
 TGCACCTGCA TAAACTTAGG TAAATGATCA AAAATGAAGT TGATGGGAAC TTAAAACCGC 300
 CCTGAAGTAA AGCTAGGAAT AGTCATATAA TGTCACCTT TGGTGTCTGC GCTAACATCA 360
30 ACAACAACAT ACCTCGTGTA GTCCACAAA GTGGTTTCAG GGGGAGGGTA GAGTGTATGC 420
 AAAAC T TACT CCTATCTCAG AGGTAGAGAG GATTTTTTCA ATAGACCCCTT GGCTCAAGAA 480
35 AAAAAGTCCA AAAAGAAGTA ACAGAAGTGA AAGCAACATG TGTAGCTAAA GCGACCCAAC 540
 TTGTTTGGGA CTGAAGTAGT TGTTGTTGTT GAAACAGTGC ATGTAGATGA ACACATGTCA 600
 GAAAATGGAC AACACAGTTA TTTTGTGCAA GTCAAAAAA TGTACTACTA TTTCTTTGTG 660
40 CAGCTTTATG TATAGAAAAG TTAAATAACT AATGAATTTT GCTAGCAGAA AAATAGCTTG 720
 GAGAGAAATT TTTTATATTG AACTAAGCTA ACTATATTCA TCTTTCTTTT TGCTTCTTCT 780
 TCTCCTTGTT TGTGAAG 797

45 (2) INFORMATION FOR SEQ ID NO: 14:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2169 base pairs
50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	ATCATGGCCA ATTACTGGTT CAAATGCATT ACTTCCTTTC AGATTCTTTC GAGTTCTCAT	60
10	GACCGGTCCT ACTACAGACG ATACTAACCC GTGGAAGTGT TGCATCTGCT TCTTAGAACT	120
	CTATGGCTAT TTTCGTTAGC TTGGCGTCGG TTTGAACATA GTTTTTGTTT TCAAACCTCTT	180
	CATTTACAGT CAAAATGTTG TATGGTTTTT GTTTTCCTCA ATGATGTTTA CAGTGTGTGTG	240
15	TTGTCATCTG TACTTTTGCC TATTACTTGT TTTGAGTTAC ATGTTAAAAA AGTGTTTATT	300
	TTGCCATATT TTGTTCTCTT ATTATTATTA TCATACATAC ATTATTACAA GGAAAAGACA	360
20	AGTACACAGA TCTTAACGTT TATGTTCAAT CAACTTTTGG AGGCATTGAC AGGTACCACA	420
	AATTTTGAGT TTATGATTAA GTTCAATCTT AGAATATGAA TTAAACATCT ATTATAGATG	480
	CATAAAAATA GCTAATGATA GAACATTGAC ATTTGGCAGA GCTTAGGGTA TGGTATATCC	540
25	AACGTTAATT TAGTAATTTT TGTTACGTAC GTATATGAAA TATTGAATTA ATCACATGAA	600
	CGGTGGATAT TATATTATGA GTTGGCATCA GCAAAATCAT TGGTGTAGTT GACTGTAGTT	660
30	GCAGATTTAA TAATAAAATG GTAATTAACG GTCGATATTA AAATAACTCT CATTTCAAGT	720
	GGGATTAGAA CTAGTTATTA AAAAAATGTA TACTTTAAGT GATTTGATGG CATATAATTT	780
	AAAGTTTTTC ATTTTCATGCT AAAATTGTTA ATTATTGTAA TGTAGACTGC GACTGGAATT	840
35	ATTATAGTGT AAATTTATGC ATTCAGTGTA AAATTAAAGT ATTGAAGTTG TCTGTTTTAG	900
	AAAATACTTT ATACTTTAAT ATAGGATTTT GTCATGCGAA TTAAATTAA TCGATATTGA	960
40	ACACGGAATA CCAAATTAA AAAGGATACA CATGGCCTTC ATATGAACCG TGAACCTTTG	1020
	ATAACGTGGA AGTTCAAAGA AGGTAAAGTT TAAGAATAAA CTGACAAATT AATTTCTTTT	1080
	ATTTGGCCCA CTAATAAATT TGCTTTACTT TCTAACATGT CAAGTTGTGC CCTCTTAGTT	1140
45	GAATGATATT CATTTTTCAT CCCATAAGTT CAATTTGATT GTCATACCAC CCATGATGTT	1200
	CTGAAAAATG CTTGGCCATT CACAAAGTTT ATCTTAGTTC CTATGAACTT TATAAGAAGC	1260
50	TTTAATTTGA CATGTTATTT ATATTAGATG ATATAATCCA TGACCCAATA GACAAGTGTA	1320
	TTAATATTGT AACTTTGTAA TTGAGTGTGT CTACATCTTA TTCAATCATT TAAGGTCATT	1380
	AAAATAAATT ATTTTTTGAC ATTCTAAAC TTTAAGCAGA ATAAATAGTT TATCAATTAT	1440
55	TAAAAACAAA AAACGACTTA TTTATAAATC AACAAACAAT TTTAGATTGC TCCAACATAT	1500

TTTTCCAAAT TAAATGCAGA AAATGCATAA TTTTATACTT GATCTTTATA GCTTATTTT 1560
TTTAGCCTAA CCAACGAATA TTTGTAACT CACAACTTGA TTAAAAGGGA TTTACAACAA 1620
5 GATATATATA AGTAGTGACA AATCTTGATT TTAAATATTT TAATTTGGAG GTCAAAATTT 1680
TACCATAATC ATTTGTATTT ATAATTAAAT TTAAATATC TTATTTATAC ATATCTAGTA 1740
AACTTTTAAA TATACGTATA TACAAAATAT AAAATTATTG GCGTTCATAT TAGGTCAATA 1800
10 AATCCTTAAC TATATCTGCC TTACCACTAG GAGAAAGTAA AAAACTCTTT ACCAAAAATA 1860
CATGTATTAT GTATACAAAA AGTCGATTAG ATTACCTAAA TAGAAATTGT ATAACGAGTA 1920
15 AGTAAGTAGA AATATAAAAA AACTACAATA CTAAAAAAA TATGTTTTAC TTCAATTTTCG 1980
AAACTAATGG GGTCTGAGTG AAATATTCAG AAAGGGGAGG ACTAACAAAA GGGTCATAAT 2040
GTTTTTTTAT AAAAAGCCAC TAAAATGAGG AAATCAAGAA TCAGAACATA CAAGAAGGCA 2100
20 GCAGCTGAAG CAAAGTACCA TAATTTAATC AATGGAAATT AATTTCAAAG TTTTATCAAA 2160
ACCCATTTCG 2169

25 (2) INFORMATION FOR SEQ ID NO: 15: .

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1165 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGTCAAAGA AATTCTCGAG GTTACATGGA TATCTTGAGA ACTTAAGAAA TTTTACAGTA 60
45 TAATTGAACA AGTATATGCA GCATATCCTA ATTTCTGGAC TGACTGGTAG CCATAAACTG 120
AATTTGAATT CATAGAAATT ATTGGAGTAG CGTTTGAGCT TCTCAAGGTC CATACAAAGA 180
50 ACACATTCTC AACTATCCGT CTCATAGGAT ACAACATTTT CAATTGCAGT TCAACACCAA 240
AAAAATGTAA AAAATAGAAA CATCATGACC AGGTAATCAA AACATACTCG TTCGATACGG 300
AATCTATTAT TGGTACATTT AAAAGGCTAG AAAAAACAAA CTTCAGTAGC TATCTCAGCA 360
55 TTATAACTTA TTATGTTTCC AGCAAAAGCC ATAACAAATC TTATATAACT TTCACAAAGA 420

40

AACAATTTTT ATCATATCCC TGGACATATA ATGAACCCTT TATGTGTTCA GAACTTTGCC 480
CTTGACCATG TATTTGTGTT GTAAAAAATC CACTTATTAT GTATACATAA TTGATTTACA 540
5 ACAACAAACA CAATGTAATC CCACAAGTGG AGTGTGGTGA GGACTTTACC CCTACCTTAC 600
GAGATAGAGA GATTGTTTCT AATAGACCCT CGGCTAAAGT AAAAGCATTT CAAAGCAACG 660
CGAATATAAA GAAGGCATGA TAAACACTA AAGGAAGCAT GCTAGAGCAT TCTTACCGAG 720
10 GAACAATAAC TACGACAAGA TATATAATAC AATAATCGAA GTACAAGAAA CAGAAAAATAG 780
AATAACAAAG ATCAAATAAC AAAACAAGAA ACTACCCAAA TAATTCCACG ACTACTAGTA 840
15 TGAAAGGATA AGCCAGACAA CACTCAAATA CCTAACTAAC CTTCTACCCC TCATCCGTGT 900
CCTCCATAAC CTCCTAGAAC ACTCTTTCTA AATATTGTCT TCCCCACCC CCCCTCCATC 960
TCTCAATTTT TGAATTTTAT AACTCAACC ACCTTGCAA TTTGTCACAT GATACTTACA 1020
20 TATGGCTCTA CAAGTGTCT TTTTCTTCCA TATTGATAT TATAAAAAAT AAAATAAAAA 1080
ACTAAGGAGA TGATCCAGAT ATATTGAAA ATGAAATGCA AAGGCTAAAA ATAATTGAAA 1140
25 TTAACATGAA ATTAGTAAAA ATTAC 1165

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: YES

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCAAGCAATG CACCACAGTT AGTTTATATC AAAAAGAAGA AAGGTATTAA CGGAGCTAAA 60
AACTGTTATA TACCACATGA AAGAAGTTGA TAATGTGAAA ACACCATGCT CATAAAGATT 120
50 GTAATTCAAA TAACAAATGC CCACAGGAGT AAAGAGCTGT CTTTCCAAG TTAAGGTATT 180
ATAAATTGGC GGAACGAAGT AACACATGTT TGACATCTCC ACACGGTGCA CAGATCAAAT 240
ATGCCATGAG CACCAGTCCA GAAGTTTTC AACTATTTAT ATACTATCCA TGCAACCATA 300
55 TAAATTATCA AACATAC 317

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTGCAAAAAA AGAGAGCAGT TTACACAAGA AAAAAGTCTT AAATCTCAAC AAAAGTATCA 60
TGAATTTAAT ATTAAGGAAG CTATTTTCGAA CAGAAAGAGT AACTCATGAT AATAGAAGGA 120
AATTGTGAAG CAACAGAAGG AAGACTTTCT TTATTTCTAC AAAATTGCTT TAAGACTATA 180
TTTGATGCTT GTATAGTACA TGTGTAATCC CCTCAGCTTC TTTATGTCTA TACTTTTTTTT 240
ATATTTTGAA TCTCCTTAGT GAAAATCTTT GCTTTGCCAC TGACACTCCG GGGGTGTGTC 300
ACTTCTCCAA AAACCTTGTC TACTTTTTTTG AAGACCCAAT CAAACAGCTT TTAAAAAGAT 360
CAAAAAAATG GCCAGGTGCC ACCTAAATGG AGCCACTACT TACTCCCCGG TATGCAAAAT 420
TCTCTAGCAA AGTCAAAGTA GGTATAACA ATTATCTTC CAAAATAAGG TCAAAGTACC 480
TAAAGCACAA CTTTGGCTG TTAC 504

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTGCATTGTG GATGAGTTAA TTAGAAGCAT AACCTTAATA GCAATTAGAA CATGTAAGAA 60

AGCCAATGAT GCTGCAACAT CATGCTTTAA TAGGAAAATC TGTTATGATG ATGGAAACTA 120
CTATTTTGTA GTAGACGAGG ACCTAC 146

5 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
15 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

25 CTGTTTAATT GCTGAAGTAG TAAGTTCTCA AGCACTTATA GAATTGACTC ATTTTGTTAA 60
GGGAAAGAGT ATGGGATCAA GTCCAAATTA GTAAAGACAC AATTATTTTA ACTTTTGCAT 120
TTCAAAATGT CTTACATAAC AAGACTAGTA AGAACATGAA TCGAAATGCC TGTGATGATG 180
30 GTGTTCAAAA TTCAGCTTCA AGGTATGAAT AACAAAAC 218

(2) INFORMATION FOR SEQ ID NO: 20:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
45 (iv) ANTI-SENSE: YES

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTGTATCCAG CAGACATAAT AGGAGTGAAC ATAAAAATGT CACTGGATAA ATAACTTATC 60
ATGATATTCA GCGGCTACCA ATATTCTGAA GGCCCATGGC GAAAATAAGT ACTTTTATAC 120
55 TTTCAGGACG TATATATTTG GATTCTATCT AACCAATTGTT CTGAGAATTA TTTAGTTGTA 180

GAAATAAATT TAAAATAC

198

(2) INFORMATION FOR SEQ ID NO: 21:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: YES

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGTGGTTAG AAGCTAAAAG TGAATAGATG AGAAAAATTA CCTCCAAATA AGAGGGATAT 60
TGAAAAAGAA ACACAATGCA TGAAAAGAAT AAACAAATGA TAAACGAGAA AATTGAATAA 120
25 TCCATCAGAA CCCTGGTTAC CTCACAAAGA GTGAGATTTT CCGTGGCTAA CCTATATGAA 180
CCTTAAATG CAATAGAAAC AGACAAAC 208

30 (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 40 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CTGTACAAGT TCATCAAACA TTTCACAATT ACTCCAAAAC AGACACACTT GCAAACCTCTA 60
50 TACAGTAATC TTCTATACTA CAAAAAAGTA AACAATGTTT TTTTAAAGAT GACATTTGTT 120
CTCAGCAACA TAATAGAAAT CCCTAGACAA TGGAACATT CATCATGTTG TTTTCCTCTA 180
55 TGTTTCAACC CCTTTGATGT TCAACAGTTC AGGTCATTTT GAGGAATGAA TCTTGTTCAA 240
GTAAGCCAAA CTAATTGTAA TTATCACAAA ATATCTAAAG ATGTAAGACA TAC 293

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

20 CTGCATTTCA TCATGAGGGG GAGGAAAGAC GGAGAAATAT AGATATCAGA TTTAGACCAT 60
TTCAATTAGT ATCACTTCAT TGTAAGAAA AGGTAAGTAT CCAACAAATA TAGCAGGCTG 120
25 TGGATTGGTA GCCTGAACT ATAGCTTCAA AGAATCAACT TAAGCTGCTC ATCAAGGCCT 180
TAGTGGTAGA AATGAGGCGG TAATAAGTGT AAATGAATCT AATACTTGA TCTCGAAACA 240
AAAATCAGAA ATTCGGTTGG AAAATAAGTA GAACAAGATG AAATGAGCTA TCATCCCCAG 300
30 AACCAAGTAG ACTTCCAAGT AAGCAATCTA AAAATTACTA GATTATTTAA CAAGCTGCGA 360
TTCAAAATAC TTGAAC 376

35 (2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

55 CTGCAAAGTG AAGTAACTAA TCAGTACAGC TATTACCGAA TTTGACCAGC TATTGGATTA 60
AATAATATGA AATCCATCAT CAAGAAATGG AAGGTAAAAA GGTTTCTACT TGTCCTTGGA 120

45

TAGAATTAAA GCACTTCATA AACCCAACAC TTTCAACTTT AGATGATTTT AC 172

(2) INFORMATION FOR SEQ ID NO: 25:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: YES

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CTGTTTTCGT CATGCGAGGA TCAGAAAAA GAGTTAAATT AGACAATGTG AAAATGATTT 60

GTTTCAGTTA CTTCTCCATA AACTTGTTT AGTACATTAA AAACAAGCAG AGCAATAATT 120

25 TCATGGATAA GTAAACATA TATAC 145

(2) INFORMATION FOR SEQ ID NO: 26:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: YES

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:⁴ 26:

CTGTCATGAG AACAGATTGT ATGTCAGCAT GAAGACAAAG ATCATCAATA AACAGTTTTC 60

TCCTTTTGA ATTAGCTAAA CAACGCAGGG GGAGGGCAGG AGGCTCAAAC ACTTCCGAAC 120

50 TCAGACAGTC GGATATCTTA TACAACTAAA GATGGATGAG ACAATTACAG TTCTTTTGG 180

TGAGAGAACT GTACCCTACA TCTGTTATCT TATTATCAAA AGTTATTCAA GCAAATCCTT 240

55 AC 242

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTTCACAAAC AAGGAGAAGA AGAAGCAAAA AGAAAGATGA ATATAGTTAG CTTAGTTCAA	60
TATAAAAAAT TTCTCTCCAA GCTATTTTTT TGCTAGCAAA ATTCATTAGT TATTTAACTT	120
TTCTATACAT AAAGCTGCAC AAAGAAATAG TAGTACATTT TTTTGACTTG CACAAAATAA	180
CTGTGTTGTC CATTTTCTGA CATGTGTTCA TCTACATGCA CTGTTTCAAC AACACAACCT	240
ACTTCAGTCC CAAACAAGTT GGGTCGCTTT AGCTACACAT GTTGCTTTCA CTTCTGTTAC	300
TTCTTTTTGG ACTTTTTTTC TTGAGCCAAG GGTCTATTGA AAAAATCCTC TCTACCTCTG	360
AGATAGGAGT AAGTTTGTGA TACACTCTAC CCTCCCCCTG AAACCACTTT GTGGGACTAC	420
ACGAGGTATG TTGTTGTTGA TGTTAGCGCA GACACCAAAG GTGGACATTA TATGACTATT	480
CCTAGCTTTA CTTCAGGGCG GTTTTAAGTT CCCATCAACT TCATTTTGA TCATTTACCT	540
AAGTTTATGC AGGTGCAAGC TACATGCACT GGTTTAGGGA AAAAGAGGAT AGAGAAGAAT	600
TTTTTTGGCA TCCTTTTGTT TTGTAACAGT AAGATGCCAA AAGTAGACCT TATTACGGCT	660
ATTCCTACCT TTCAAATTAG TAGTTCAGAG GACTTAACTG GCGATTGTGG CGGTAATCAA	720
TAGTTAACTT CTATCGCATT CAAATAACTA TGAACAAAAC CACAATAAAA AGGGAGGTCA	780
CACGGCAAGA ACTGTAC	797

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

10	CGAATGGGTT TTGATAAAAC TTTGAAATTA ATTTCCATTG ATTAAATTAT GGTACTTTGC	60
	TTCAGCTGCT GCCTTCTTGT ATGTTCTGAT TCTTGATTTC CTCATTTTAG TGGCTTTTAA	120
	TAAAAAACA TTATGACCCT TTTGTTAGTC CTCCCCTTTC TGAATATTTT ACTCAGACCC	180
15	CATTAGTTTC GAAATTGAAG TAAAACATAT TTTTTTAGT ATTGTAGTTT TTTTATATTT	240
	CTACTTACTT ACTCGTTATA CAATTTCTAT TTAGGTAATC TAATCGACTT TTTGTATACA	300
	TAATACATGT ATTTTGGTA AAGAGTTTTT TACTTCTCC TAGTGGTAAG GCAGATATAG	360
20	TTAAGGATTT ATTGACCTAA TATGAACGCC AATAATTTTA TATTTGTAT ATACGTATAT	420
	TTAAAAGTTT ACTAGATATG TATAAATAAG ATATTTAAAA TTTAATTATA AATACAAATG	480
25	ATTATGGTAA AATTTTGACC TCCAAATTAA AATATTTAAA ATCAAGATTT GTCACTACTT	540
	ATATATATCT TGTGTAAAT CCCTTTTAAT CAAGTTGTGA GTTTACAAAT ATTCGTTGGT	600
	TAGGCTAAAA AAAATAAGCT ATAAAGATCA AGTATAAAAT TATGCATTTT CTGCATTTAA	660
30	TTTGAAAAA TATGTTGGAG CAATCTAAAA TTGTTTGTG ATTTATAAAT AAGTCGTTTT	720
	TTGTTTTTAA TAATTGATAA ACTATTTATT CTGCTTAAAG TTTTAGAATG TCAAAAAATA	780
35	ATTTATTTTA ATGACCTTAA ATGATTGAAT AAGATGTAGA CACACTCAAT TACAAAGTTA	840
	CAATATTAAT ACACTTGTCT ATTGGGTCAT GGATTATATC ATCTAATATA AATAACATGT	900
	CAAATTAAAG CTCTTATAA AGTTCATAGG AACTAAGATA AACTTTGTGA ATGGCCAAGC	960
40	ATTTTTCAGA ACATCATGGG TGGTATGACA ATCAAATTGA ACTTATGGGA TGAAAAATGA	1020
	ATATCATTCA ACTAAGAGGG CACAACTTGA CATGTTAGAA AGTAAAGCAA ATTTAGTAGT	1080
45	GGGCCAAATA AAAGAAATTA ATTTGTCAGT TTATTCTTAA ACTTTACCTT CTTTGAACCT	1140
	CCACGTTATC AAAGGTTTAC GGTTCATATG AAGGCCATGT GTATCCTTTT TAATTTTGGT	1200
	ATTCCTGTGTT CAATATCGAT TAATTTAAAT TCGCATGACA AAATCCTATA TTAAAGTATA	1260
50	AAGTATTTTC TAAAACAGAC AAGTTCAATA CTTTAATTTT AACTGAATG CATAAATTTA	1320
	CACTATAATA ATTCAGTCG CAGTCTACAT TACAATAATT AACAAATTTA GCATGAAATG	1380
55	AAAACTTTA AATTATATGC CATCAAATCA CTAAAGTAT ACATTTTTTT AATAACTAGT	1440
	TCTAATCCCA CTTGAAATGA GAGTTATTTT AATATCGACC GTTAATTACC ATTTTATTAT	1500

TAAATCTGCA ACTACAGTCA ACTACACCAA TGATTTTGCT GATGCCAACT CATAATATAA 1560
 TATCCACCGT TCATGTGATT AATCAATAT TTCATATACG TACGTAACAA AAATTACTAA 1620
 5 ATTAACGTTG GATATACCAT ACCCTAAGCT CTGCCAAATG TCAATGTTCT ATCATTAGCT 1680
 ATTTTATGC ATCTATAATA GATGTTAAAT TCATATTCTA AGATTGAACT TAATCATAAA 1740
 10 CTCAAATTT GTGGTACCTG TCAATGCCTC CAAAAGTTGA TTGAACATAA ACGTTAAGAT 1800
 CTGTGTACTT GTCTTTCCT TGTAATAATG TATGTATGAT AATAATAATA AGAGAACAAA 1860
 ATATGGCAAA ATAAACACTT TTTTAACATG TAACTCAAAA CAAGTAATAG GCAAAAAGTAC 1920
 15 AGATGACAAC ACAACACTGT AAACATCATT GAGGAAAACA AAAACCATAC AACATTTTGA 1980
 CTGTAAATGA AGAGTTTGAA AACAAAAACT ATGTTCAAAC CGACGCCAAG CTAACGAAAA 2040
 20 TAGCCATAGA GTTCTAAGAA GCAGATGCAA CAGTTCCACG GGTTAGTATC GTCTGTAGTA 2100
 GGACCGGTCA TGAGAACTCG AAAGAATCTG AAAGGAAGTA ATGCATTTGA ACCAGTAATT 2160
 GGCCATGAT 2169
 25

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

45 ATCATGGCCA ATTACTGGTT CAAATGCATT ACTTCCTTTC AGATTCTTTC GAGTTCTCAT 60
 GACCGGTCCT ACTACAGACG AACTAACCC GTGGAAGTGT TGCATCTGCT TCTTAGAACT 120
 CTATGGCTAT TTTCGTTAGC TTGGCGTCGG TTTGAACATA GTTTTGTGTT TCAAACCTCTT 180
 50 CATTTACAGT CAAAATGTTG TATGGTTTTT GTTTTCCTCA ATGATGTTTA CAGTGTGTGTG 240
 TTGTCATCTG TACTTTTGCC TATTACTTGT TTTGAGTTAC ATGTTAAAAA AGTGTATTATT 300
 55 TTGCCATATT TTGTTCTCTT ATTATTATTA TCATACATAC ATTATTACAA GGAAAAGACA 360
 AGTACACAGA TCTTAACGTT TATGTTCAAT CAACTTTTGG AGGCATTGAC AGGTACCACA 420

	AATTTTGAGT TTATGATTAA GTTCAATCTT AGAATATGAA TTTAACATCT ATTATAGATG	480
	CATAAAAATA GCTAATGATA GAACATTGAC ATTTGGCAGA GCTTAGGGTA TGGTATATCC	540
5	AACGTTAATT TAGTAATTTT TGTTACGTAC GTATATGAAA TATTGAATTA ATCACATGAA	600
	CGGTGGATAT TATATTATGA GTTGGCATCA GCAAATCAT TGGTGTAGTT GACTGTAGTT	660
10	GCAGATTTAA TAATAAAATG GTAATTAACG GTCGATATTA AAATAACTCT CATTTCAAGT	720
	GGGATTAGAA CTAGTTATTA AAAAAATGTA TACTTTAAGT GATTTGATGG CATATAATTT	780
	AAAGTTTTTC ATTTTCATGCT AAAATTGTGA ATTATTGTAA TGTAGACTGC GACTGGAATT	840
15	ATTATAGTGT AAATTTATGC ATTCAAGTGA AAATTAAAGT ATTGAAGTTG TCTGTTTTAG	900
	AAAATACTTT ATACTTTAAT ATAGGATTTT GTCATGCGAA TTTAAATTAA TCGATATTGA	960
20	ACACGGAATA CCAAAATTAA AAAGGATACA CATGGCCTTC ATATGAACCG TGAACCTTTG	1020
	ATAACGTGGA AGTTCAAAGA AGGTAAAGTT TAAGAATAAA CTGACAAATT AATTTCTTTT	1080
	ATTTGGCCCA CTAATAAATT TGCTTTACTT TCTAACATGT CAAGTTGTGC CCTCTTAGTT	1140
25	GAATGATATT CATTTTTTCAT CCCATAAGTT CAATTTGATT GTCATACCAC CCATGATGTT	1200
	CTGAAAAATG CTTGGCCATT CACAAAGTTT ATCTTAGTTC CTATGAACCT TATAAGAAGC	1260
30	TTTAATTTGA CATGTTATTT ATATTAGATG ATATAATCCA TGACCCAATA GACAAGTGTA	1320
	TTAATATTGT AACTTTTGTA TTAGTGTGT CTACATCTTA TTCAATCATT TAAGGTCATT	1380
	AAAATAAATT ATTTTTTGAC ATTCTAAAAC TTTAAGCAGA ATAAATAGTT TATCAATTAT	1440
35	TAAAAACAAA AAACGACTTA TTTATAAATC AACAAACAAT TTTAGATTGC TCCAACATAT	1500
	TTTTCCAAAT TAAATGCAGA AAATGCATAA TTTTATACTT GATCTTTATA GCTTATTTTT	1560
40	TTTAGCCTAA CCAACGAATA TTTGTAACT CACAACTTGA TTAAAAGGGA TTTACAACAA	1620
	GATATATATA AGTAGTGACA AATCTTGATT TTAAATATTT TAATTTGGAG GTCAAAATTT	1680
	TACCATAATC ATTTGTATTT ATAATTAAAT TTTAAATATC TTATTTATAC ATATCTAGTA	1740
45	AACTTTTAAA TATACGTATA TACAAAATAT AAAATTATTG GCGTTCATAT TAGGTCAATA	1800
	AATCCTTAAC TATATCTGCC TTACCACTAG GAGAAAGTAA AAAACTCTTT ACCAAAAATA	1860
50	CATGTATTAT GTATACAAAA AGTCGATTAG ATTACCTAAA TAGAAATTGT ATAACGAGTA	1920
	AGTAAGTAGA AATATAAAAA AACTACAATA CTAAAAAAA TATGTTTTAC TTCAATTTTCG	1980
	AACTAATGG GGTCTGAGTG AAATATTGAG AAAGGGGAGG ACTAACAAAA GGGTCATAAT	2040
55	GTTTTTTTAT AAAAAGCCAC TAAAATGAGG AAATCAAGAA TCAGAACATA CAAGAAGGCA	2100

	GCAGCTGAAG	CAAAGTACCA	TAATTTAATC	AATGGAAATT	AATTTCAAAG	TTTTATCAAA	2160
	ACCCATTCTGA	GGATCTTTTC	CATCTTTCTC	ACCTAAAGTT	TCTTCAGGGG	TAATTTTAC	2220
5	TAATTTTCATG	TTAATTTCAA	TTATTTTATG	CCTTTGCATT	TCATTTTCCA	ATATATCTGG	2280
	ATCATCTCCT	TAGTTTTTTA	TTTTATTTT	TATAATATCA	AATATGGAAG	AAAAATGACA	2340
	CTTGTTAGAGC	CATATGTAAG	TATCATGTGA	CAAATTTGCA	AGGTGGTTGA	GTGTATAAAA	2400
10	TTCAAAAATT	GAGAGATGGA	GGGGGGGTGG	GGGAAGACAA	TATTTAGAAA	GAGTGTCTA	2460
	GGAGGTTATG	GAGGACACGG	ATGAGGGGTA	GAAGGTTAGT	TAGGTATTTG	AGTGTGTCT	2520
15	GGCTTATCCT	TTCATACTAG	TAGTCGTGGA	ATTATTTGGG	TAGTTTCTTG	TTTTGTTATT	2580
	TGATCTTTGT	TATTCTATTT	TCTGTTTCTT	GTAATTCGAT	TATTGTATTA	TATATCTTGT	2640
	CGTAGTTATT	GTTCTCGGT	AAGAATGCTC	TAGCATGCTT	CCTTTAGTGT	TTTATCATGC	2700
20	CTTCTTTATA	TTGCGGTTGC	TTTGAAATGC	TTTTACTTTA	GCCGAGGGTC	TATTAGAAAC	2760
	AATCTCTCTA	TCTCGTAAGG	TAGGGGTAAA	GTCCTCACCA	CACTCCACTT	GTGGGATTAC	2820
25	ATTGTGTTTG	TTGTTGTAAA	TCAATTATGT	ATACATAATA	AGTGGATTTT	TTACAACACA	2880
	AATACATGGT	CAAGGGCAAA	GTTCTGAACA	CATAAAGGGT	TCATTATATG	TCCAGGGATA	2940
	TGATAAAAAT	TGTTTCTTTG	TGAAAGTTAT	ATAAGATTTG	TTATGGCTTT	TGCTGGAAAC	3000
30	ATAATAAGTT	ATAATGCTGA	GATAGCTACT	GAAGTTTGTT	TTTTCTAGCC	TTTTAAATGT	3060
	ACCAATAATA	GATTCCGTAT	CGAACGAGTA	TGTTTTGATT	ACCTGGTCAT	GATGTTTCTA	3120
35	TTTTTTACAT	TTTTTTGGTG	TTGAACTGCA	ATTGAAAATG	TTGTATCCTA	TGAGACGGAT	3180
	AGTTGAGAAT	GTGTTCTTTG	TATGGACCTT	GAGAAGCTCA	AACGCTACTC	CAATAATTC	3240
	TATGAATTCA	AATTCAGTTT	ATGGCTACCA	GTCAGTCCAG	AAATTAGGAT	ATGCTGCATA	3300
40	TACTTGTTCA	ATTATACTGT	AAAATTTCTT	AAGTTCTCAA	GATATCCATG	TAACCTCGAG	3360
	AATTTCTTTG	ACAGGCTTCT	AGAAATAAGA	TATGTTTTCC	TTCTCAACAT	AGTACTGGAC	3420
45	TGAAGTTTGG	ATCTCAGGAA	CGGTCTTGGG	ATATTTCTTC	CACCCCAAAA	TCAAGAGTTA	3480
	GAAAAGATGA	AAGGGTATGT	TTGATAATTT	ATATGGTTGC	ATGGATAGTA	TATAAATAGT	3540
	TGGAAACTT	CTGGACTGGT	GCTCATGGCA	TATTTGATCT	GTGCACCGTG	TGGAGATGTC	3600
50	AAACATGTGT	TACTTCGTTT	CGCCAATTTA	TAATACCTTA	ACTTGGGAAA	GACAGCTCTT	3660
	TACTCCTGTG	GGCATTGTGT	ATTTGAATTA	CAATCTTTAT	GAGCATGGTG	TTTTACATT	3720
55	ATCAACTTCT	TTCATGTGGT	ATATAACAGT	TTTTAGCTCC	GTTAATACCT	TTCTTCTTTT	3780
	TGATATAAAC	TAACTGTGGT	GCATTGCTTG	CATGAAGCAC	AGTTCAGCTA	TTCCGCTGT	3840

	TTTGACCGAT GACGACAATT CGACAATGGC ACCCCTAGAG GAAGATGTCA AGACTGAAAA	3900
	TATTGGCCTC CTAAATTTGG ATCCAACCTT GGAACCTTAT CTAGATCACT TCAGACACAG	3960
5	AATGAAGAGA TATGTGGATC AGAAAATGCT CATTGAAAAA TATGAGGGAC CCCTTGAGGA	4020
	ATTTGCTCAA GGTAACAGCC AAAAGTTGTG CTTTAGGCAG TTTGACCTTA TTTTGGAAGA	4080
10	TGAATTGTTT ATACCTACTT TGACTTTGCT AGAGAATTTT GCATACCGGG GAGTAAGTAG	4140
	TGGCTCCATT TAGGTGGCAC CTGGCCATT TTTTGATCTT TTAAAAAGCT GTTTGATTGG	4200
	GTCTTCAAAA AAGTAGACAA GGTTTTTGGA GAAGTGACAC ACCCCCGGAG TGTCAGTGGC	4260
15	AAAGCAAAGA TTTTCACTAA GGAGATTCAA AATATAAAAA AAGTATAGAC ATAAAGAAGC	4320
	TGAGGGGATT CAACATGTAC TATACAAGCA TCAAATATAG TCTTAAAGCA ATTTTGTAGA	4380
20	AATAAAGAAA GTCTTCCTTC TGTGCTTCA CAATTCCTT CTATTATCAT GAGTTACTCT	4440
	TTCTGTTTGA AATAGCTTCC TTAATATTAA ATTCATGATA CTTTGTGTTGA GATTTAGCAG	4500
	TTTTTCTTG TGTAAGTGC TCTCTTTTTT TGCAGTTAT TTAAATTTG GATTCAACAG	4560
25	GGAAGATGGT TGCATAGTCT ATCGTGAATG GGCTCCTGCT GCTCAGTAGG TCCTCGTCTA	4620
	CTACAAAATA GTAGTTTCCA TCATCATAAC AGATTTTCCT ATTAAAGCAT GATGTTGCAG	4680
30	CATCATGGC TTTCTTACAT GTTCTAATTG CTATTAAGGT TATGCTTCTA ATTAACATCAT	4740
	CCACAATGCA GGAAGCAGA AGTTATTGGC GATTTCAATG GATGGAACGG TTCTAACCAC	4800
	ATGATGGAGA AGGACCAGTT TGGTGTGTTGG AGTATTAGAA TTCCTGATGT TGACAGTAAG	4860
35	CCAGTCATTC CACACAATC CAGAGTTAAG TTTCGTTTCA AACATGGTAA TGGAGTGTGG	4920
	GTAGATCGTA TCCCTGCTTG GATAAAGTAT GCCACTGCAG ACGCCACAAA GTTTCAGCA	4980
40	CCATATGATG GTGTCTACTG GGACCCACCA CCTTCAGAAA GGTTTGTGTA TTCATACCTT	5040
	GAAGCTGAAT TTTGAACACC ATCATCACAG GCATTTTCGAT TCATGTTCTT ACTAGTCTTG	5100
	TTATGTAAGA CATTTTGAAA TGCAAAAGTT AAAATAATTG TGTCTTTACT AATTTGGACT	5160
45	TGATCCCATA CTCTTCCCT TAACAAAATG AGTCAATTCT ATAAGTGCTT GAGAACTTAC	5220
	TACTTCAGCA ATTAAACAGG TACCACTTCA AATACCCTCG CCCTCCCAA CCCCAGCCC	5280
50	CACGAATCTA TGAAGCACAT GTCGGCATGA GCAGCTCTGA GCCACGTGTA AATTCGTATC	5340
	GTGAGTTTGC AGATGATGTT TTACCTCGGA TTAAGGCAAA TAACTATAAT ACTGTCCAGT	5400
	TGATGGCCAT AATGGAACAT TCTTACTATG GATCATTTGG ATATCATGTT ACAAACCTTT	5460
55	TTGCTGTGAG CAGTAGATAT GGAAACCCGG AGGACCTAAA GTATCTGATA GATAAAGCAC	5520

	ATAGCTTGGG	TTTACAGGTT	CTGGTGGATG	TAGTTCACAG	TCATGCAAGC	AATAATGTCA	5580
	CTGATGGCCT	CAATGGCTTT	GATATTGGCC	AAGGTTCTCA	AGAATCCTAC	TTTCATGCTG	5640
5	GAGAGCGAGG	GTACCATAAG	TTGTGGGATA	GCAGGCTGTT	CAACTATGCC	AATTGGGAGG	5700
	TTCTTCGTTT	CCTTCTTTCC	AACTTGAGGT	GGTGGCTAGA	AGAGTATAAC	TTTGACGGAT	5760
10	TTCGATTTGA	TGGAATAACT	TCTATGCTGT	ATGTTTATCA	TGGAATCAAT	ATGGGATTTA	5820
	CAGGAAACTA	TAATGAGTAT	TTCAGCGAGG	CTACAGATGT	TGATGCTGTG	GTCTATTTAA	5880
	TGTTGGCCAA	TAATCTGATT	CACAAGATTT	TCCCAGATGC	AACTGTTATT	GCCGAAGATG	5940
15	TTTCTGGTAT	GCCGGGCCTT	GGCCGGCCTG	TTTCTGAGGG	AGGAATTGGT	TTTGTTTACC	6000
	GCCTGGCAAT	GGCAATCCCA	GATAAGTGA	TAGATTATTT	AAAGAATAAG	AATGATGAAG	6060
20	ATTGGTCCAT	GAAGGAAGTA	ACATCGAGTT	TGACAAATAG	GAGATATACA	GAGAAGTGTA	6120
	TAGCATATGC	GGAGACCCAT	GATCAGGTAT	TTTAAATTTA	TTTCTACAAC	TAAATAATTC	6180
	TCAGAACAAT	TGTTAGATAG	AATCCAAATA	TATACGTCCT	GAAAGTATAA	AAGTACTTAT	6240
25	TTTCGCCATG	GGCCTTCAGA	ATATTGGTAG	CCGCTGAATA	TCATGATAAG	TTATTTATCC	6300
	AGTGACATTT	TTATGTTTAC	TCCTATTATG	TCTGCTGGAT	ACAGTCTATT	GTTGGTGACA	6360
30	AGACCATTGC	ATTTCTCCTA	ATGGACAAAG	AGATGTATTC	TGGCATGTCT	TGCTTGACAG	6420
	ATGCTTCTCC	TGTTGTTGAT	CGAGGAATTG	CGCTTCACAA	GGTTTGTCTG	TTTCTATTGC	6480
	ATTTTAAGGT	TCATATAGGT	TAGCCACGGA	AAATCTCACT	CTTTGTGAGG	TAACCAGGGT	6540
35	TCTGATGGAT	TATTCAATTT	TCTCGTTTAT	CATTGTGTTA	TTCTTTTCAT	GCATTGTGTT	6600
	TCTTTTTCAA	TATCCCTCTT	ATTTGGAGGT	AATTTTCTC	ATCTATTAC	TTTTAGCTTC	6660
40	TAACCACAGA	TGATCCATTT	TTTCACAATG	GCCTTGGGAG	GAGAGGGGTA	CCTCAATTTT	6720
	ATGGGTAACG	AGGTATGTCT	TACATCTTTA	GATATTTTGT	GATAATTACA	ATTAGTTTGG	6780
	CTTACTTGAA	CAAGATTCAT	TCCTCAAAAT	GACCTGAACT	GTTGAACATC	AAAGGGGTTG	6840
45	AAACATAGAG	GAAAACAACA	TGATGAATGT	TTCCATTGTC	TAGGGATTTC	TATTATGTTG	6900
	CTGAGAACAA	ATGTCATCTT	AAAAAAAACA	TTGTTTACTT	TTTGTTAGTA	TAGAAGATTA	6960
50	CTGTATAGAG	TTTGCAAGTG	TGTCTGTTTT	GGAGTAATTG	TGAAATGTTT	GATGAACTTG	7020
	TACAGTTTGG	CCATCCTGAG	TGGATTGACT	TCCCTAGAGA	GGGCAATAAT	TGGAGTTATG	7080
	ACAAATGTAG	ACGCCAGTGG	AACCTCGCGG	ATAGCGAACA	CTTGAGATAC	AAGGTTCAAG	7140
55	TATTTTGAAT	CGCAGCTTGT	TAAATAATCT	AGTAATTTT	AGATTGCTTA	CTTGGAAGTC	7200
	TACTTGTTTC	TGGGGATGAT	AGCTCATTTT	ATCTTGTTCT	ACTTATTTTC	CAACCGAATT	7260

	TCTGATTTTT	GTTTCGAGAT	CCAAGTATTA	GATTCATTTA	CACTTATTAC	CGCCTCATT	7320
	CTACCACTAA	GGCCTTGATG	AGCAGCTTAA	GTTGATTCTT	TGAAGCTATA	GTTTCAGGCT	7380
5	ACCAATCCAC	AGCCTGCTAT	ATTTGTTGGA	TACTTACCTT	TTCTTTACAA	TGAAGTGATA	7440
	CTAATTGAAA	TGGTCTAAAT	CTGATATCTA	TATTTCTCCG	TCTTTCCTCC	CCCTCATGAT	7500
10	GAAATGCAGT	TTATGAATGC	ATTTGATAGA	GCTATGAATT	CGCTCGATGA	AAAGTTCTCA	7560
	TTCCTCGCAT	CAGGAAAACA	GATAGTAAGC	AGCATGGATG	ATGATAATAA	GGTAAAATCA	7620
	TCTAAAGTTG	AAAGTGTTGG	GTTTATGAAG	TGCTTTAATT	CTATCCAAGG	ACAAGTAGAA	7680
15	ACCTTTTTAC	CTTCCATTTC	TTGATGATGG	ATTTCATATT	ATTTAATCCA	ATAGCTGGTC	7740
	AAATTCGGTA	ATAGCTGTAC	TGATTAGTTA	CTTCACTTTG	CAGGTTGTTG	TGTTTGAACG	7800
20	TGGTGACCTG	GTATTTGTAT	TCAACTTCCA	CCCAAAGAAC	ACATACGAAG	GGTATATATG	7860
	TTTACTTAT	CCATGAAATT	ATTGCTCTGC	TTGTTTTTAA	TGTACTGAAC	AAGTTTTATG	7920
	GAGAAGTAAC	TGAAACAAAT	CATTTTCACA	TTGTCTAATT	TAACCTTTTT	TTCTGATCCT	7980
25	CGCATGACGA	AAACAGGTAT	AAAGTTGGAT	GTGACTTGCC	AGGGAAGTAC	AGAGTTGCAC	8040
	TGGACAGTGA	TGCTTGGGAA	TTTGGTGGCC	ATGGAAGAGT	AAGGATTTGC	TTGAATAACT	8100
30	TTTGATAATA	AGATAACAGA	TGTAGGTGAC	AGTTCTCTCA	CCAAAAAGAA	CTGTAATTGT	8160
	CTCATCCATC	TTTAGTTGTA	TAAGATATCC	GA CTGTCTGA	GTT CGGAAGT	GTTTGAGCCT	8220
	CCTGCCCTCC	CCCTGCGTTG	TTTAGCTAAT	TCAAAAAGGA	GAAAACTGTT	TATTGATGAT	8280
35	CTTTGTCTTC	ATGCTGACAT	ACAATCTGTT	CTCATGACAG	ACTGGTCATG	ATGTTGACCA	8340
	TTTCACATCA	CCAGAAGGAA	TACCTGGAGT	TCCAGAAACA	AATTTCAATG	GTCGTCCAAA	8400
40	TTCCTTCAAA	GTGCTGTCTC	CTGCGCGAAC	ATGTGTGGTA	CAGTTCTTGC	CGTGTGACCT	8460
	CCCTTTTTAT	TGTGGTTTTG	TTCATAGTTA	TTTGAATGCG	ATAGAAGTTA	ACTATTGATT	8520
	ACCGCCACAA	TCGCCAGTTA	AGTCCTCTGA	ACTACTAATT	TGAAAGGTAG	GAATAGCCGT	8580
45	AATAAGGTCT	ACTTTTGGCA	TCTTACTGTT	ACAAAACAAA	AGGATGCCAA	AAAAATTCTT	8640
	CTCTATCCTC	TTTTTCCCTA	AACCAGTGCA	TGTAGCTTGC	ACCTGCATAA	ACTTAGGTAA	8700
50	ATGATCAAAA	ATGAAGTTGA	TGGGAACCTA	AAACCGCCCT	GAAGTAAAGC	TAGGAATAGT	8760
	CATATAATGT	CCACCTTTGG	TGTCTGCGCT	AACATCAACA	ACAACATACC	TCGTGTAGTC	8820
	CCACAAAGTG	GTTTCAGGGG	GAGGGTAGAG	TGTATGCAAA	ACTTACTCCT	ATCTCAGAGG	8880
55	TAGAGAGGAT	TTTTTCAATA	GACCCTTGGC	TCAAGAAAAA	AAGTCCAAAA	AGAAGTAACA	8940

	GAAGTGAAAG	CAACATGTGT	AGCTAAAGCG	ACCCAACTTG	TTTGGGACTG	AAGTAGTTGT	9000
	TGTTGTTGAA	ACAGTGCATG	TAGATGAACA	CATGTCAGAA	AATGGACAAC	ACAGTTATTT	9060
5	TGTGCAAGTC	AAAAAAATGT	ACTACTATTT	CTTTGTGCAG	CTTTATGTAT	AGAAAAGTTA	9120
	AATAACTAAT	GAATTTTGCT	AGCAGAAAAA	TAGCTTGGAG	AGAAATTTT	TATATTGAAC	9180
	TAAGCTAACT	ATATTCATCT	TTCTTTTTCG	TTCTTCTTCT	CCTTGTTTGT	GAAGGCTTAT	9240
10	TACAGAGTTG	ATGAACGCAT	GTCAGAAACT	GAAGATTACC	AGACAGACAT	TTGTAGTGAG	9300
	CTACTACCAA	CAGCCAATAT	CGAGGAGAGT	GACGAGAAAC	TTAAAGATTC	GTTATCTACA	9360
15	AATATCAGTA	ACATTGACGA	ACGCATGTCA	GAACTGAAG	TTTACCAGAC	AGACATTTCT	9420
	AGTGAGCTAC	TACCAACAGC	CAATATTGAG	GAGAGTGACG	AGAAACTTAA	AGATTCGTTA	9480
	TCTACAAATA	TCAGTAACAT	TGATCAGACT	GTTGTAGTTT	CTGTTGAGGA	GAGAGACAAG	9540
20	GAACCTAAAG	ATTCACCGTC	TGTAAGCATC	ATTAGTGATG	TTGTTCCAGC	TGAATGGGAT	9600
	GATTCAGATG	CAAACGTCTG	GGGTGAGGAC	TAGTCAGATG	ATTGATCGAC	CCTTCTACCG	9660
25	ATTGGTGATC	GCTATCCTTG	CTCTCTGAGA	AATAGGTGAG	GCGAAACAAA	AAATAATTTG	9720
	CATGATAAAA	AGTCTGATTT	TATGATCGCT	ATCCTCGCTC	TCTGAGAAAG	AAGCGAAACA	9780
	AAGGCGACTC	CTGGACTCGA	ATCTATAAGA	TAACAAAGGC	GACTCCTGGG	ACTCGAATCT	9840
30	ATAAGATAAC	AAAGGCAATT	CCAAGACTTG	AATCTATAAA	AAATTTAGTT	AAGAATGATT	9900
	AACGTCCGAT	CCTAATTCGA	ATCGAGGCAT	CTTACCACTC	CATTGATAAT	TATATAAGTC	9960
35	AATAAGTCAT	ATAAAGTATT	AAAAACTAAA	TTGACTTGAT	CGGTCTATCA	AAAATAGATA	10020
	AATTGTGTTT	ATATGTAACA	TTTTTGTTGT	CACAATTAGC	TTAATTACAT	CTTTCATGTG	10080
	CAATAACAAA	GAAATGATAG	GAATTTAGAG	ATTCCAATTT	TTTGTTGCC	ACAATTAAC	10140
40	TAATTACATC	TTTCATTTGC	AATAACAAAG	AAATGATAGG	AATTTAGAGA	TCCAGTGTCA	10200
	ATACACAACC	TAGGCCAACA	TCGAAAGCAT	AACGTGTAAC	TCATGCATGA	AGAAATCAGT	10260
45	CGTAAAAATG	AATAAATGCG	ACATAAAAAAC	AAATTGCATG	TATCATTAA	GTGACTTAAC	10320
	TACAAGTAAA	AATAAATTTA	ACAAATGTAA	CTTAACCTACA	AGTAAAAATA	AATTGCTTCT	10380
	ATCATTAAACA	AACAAACAGA	ATTAAAAAGA	AAAAAACATA	CTAAATCTTA	CCGTCATTCTG	10440
50	ATAAAAAAAA	ATACCAAATT	CATAATGCAA	GGAAACGAA	ACGCGTCCTG	ATCGGGTATC	10500
	AACGATGAAA	TGGACCAAGT	GGATCGACTG	CCTGCACAAC	GTTAGGTATG	CCAAAAAAA	10560
55	GAACACGATC	CTTTGCACCC	GTTTCGATGAT	TATCAGTATG	TTCAACAAAA	AAACTTAAGT	10620
	TCATCCCAGT	GTACAACAGC	CCCAACATCT	GCCCCAAGTA	ACAAAAAACA	ACCAATTTAT	10680

CTTATTCTTA TCTGCCACAA AATAATCGGT TTCACACTAT TCTCTTGTTA TACAAAATTG 10740
ACAAGTAGGA AGGAGAGGAG TCATCCAAAT AAACGGTGCA CGTTCCTTGA GAAAAGTCTT 10800
5 ATTTTTCGTA AGATCCAATT TCAACAAACT TTTCTTCAAG TCAAAATTCC TGATAGTGTA 10860
TCTCCTCTCG ACGACCTCTT GCATTGAACG ATCTCCGCTT ATCATGAAAA GTTGCTTGGA 10920
10 TAACAAGTAT TGCAAGGGGG GGACAGTAGC TATTAAAGTTA GTCGGCCCAA GGAAATGGAG 10980
GAGTGATAGT CTCGAATATT ATTCACCTCT TTAGCATTAC CCGGTCTGGC TTTAAGGAGT 11040
TACGTCTTTT ACGCTCGCCA ATTTCTTTTT TTAGAATGGT TGGTGTCAAA ATCGCGAGTT 11100
15 GTGGAAGGTT CAAGTTACTC GATTCGTGAT TTTCAAGTAT GAGTGGTGAG AGAGATTCTGA 11160
TATTTTCACG AGGTGTATTC GAGGTCTAGT AGAACGAAGG GTGTCACTAA TGAAAGTTTC 11220
20 AAGAGTTCAT CATCATCTTC TTCTAGTAGA TTTTCGCTTT CAAATGAGTA TGAAAATTCT 11280
TCCTCTTTTC TATTGATTTT CTTCAATTGT TTCTTCATTG TTGTGGTTGT TATTGAAAAG 11340
AAAGAAAATT TATAACAGAA AAAGATGTCA AAAAAAAGGT AAAATGAAAG AGTATCATAT 11400
25 ACTTAAAGAG TTGCGTAGAG ATAAGTCAAA AGAAACAGAA TTATAGTAAT TTCAGCTAAG 11460
TTAGAATTC 11469

30 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

50 GGAATTCCAG TCGCAGTCTA CATTAC

26

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
55 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single

56

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

15 CGGGATCCAG AGGCATTAAG ATTTCTGG

28

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35 CGGGATCCAA AGAAATTCTC GAGGTTACAT GG

32

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGGGATCCGG GGTAATTTT ACTAATTTCA TG

32

(2) INFORMATION FOR SEQ ID NO: 34:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CGGGATCCCG TATGTCTCAC TGTGTTTGTG GC

32

25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

45

CGGGATCCCC CTACATACAT ATATCAGATT AG

32

(2) INFORMATION FOR SEQ ID NO: 36:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

10 CCATCGATAC TTAAAGTGAT TTGATGGC 28

(2) INFORMATION FOR SEQ ID NO: 37:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

30 CGGGATCCTG TTCTGATTCT TGATTTC 28

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2122 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

55 GTATGTCTCA CTGTGTTTGT GGCTGTGTGT GTTTTTTTCT CTGTCTTTTT GTGTTTTTGT 60

TAATTGGGGC TCTTTAAAGT TGGTATTGTG TATACCCTTT TGAGTATAGT CTTTGAGGAA 120

	GCAAAATGAT GAATCTTGAT TGACATTAGT AAGGGTTGTA ACTTTTGGAA GTTTGGTTAG	180
	GTGTAATTGA GTTTGGCTTG TGTGTCTGTG TGTCGAGGTT ATTTTTTTGG TTTGTGTTAT	240
5	TGGGGATTCT TAAAAGTTGG TATTGTGTAT ACCCTTTTGA GTATAGTCTT TGAGGAAGCA	300
	AAAATGATGA ATCTTGATTG GCATTAGTAA AGGTTGTAGC TTTTGAAGT GTGGTTAGGT	360
10	GTAATTGAGT TTGGCTTG TGTCGTGTG TTTTGGAAATC CTGATGTGTG TCAAGTCCTG	420
	ATATGGGTCG AGGTTCCTTC TTTGGTTTGT GTAATTGGGG GTTCTTAAAA GTTGGTATTA	480
	TGTACCTTTT TAAGAATAGT GTCTGAGAAA GCAAAATCGA TGAATTTTGA TTGACAGCAT	540
15	ATTCTTTGAG AAAGCAAAAA ATGGTGAGTT TTCATGGAGA AACTTGATTG ACATTACTAA	600
	AGGTAGCAAC TTTTCAACT CCTGATATGG GTCAAGGTTT TTTGTTGGT TTGTGTAATT	660
20	TGGGGTTCTT TGAAGTTTTG AGAAAGAAAA ATTATGATTT TTCATGGAGA AATTTGATTT	720
	ACATTAATAA AGGTAGTAGC TTTTAAAGT GTGGTCAGCT GTAATGAGTT CAGCTTGGTT	780
	TAAAGGGGCC CTACATATGG TGCTTCTGG TGAGATATTT GTTGCTCCAC CATACGAGTT	840
25	ATAAGAATCA TAGTGTTAGG ATCTTTTTTC TTTTTTTTTT CATTTTTCAC TTGACTAGCT	900
	ACTAGAGGAG TGATCTTGAC GCGGAAAAAT CTTAGAAAGG GGAAGGTTGT TTGCATCAAC	960
30	TGGTGTTATA TGTGCAAGGA GACGGGAGAT GATGTAGATC ATCTTCTTCT TCATTGTGGT	1020
	CTTCCATGA GGTATGATG TGATATGTTT GAATGTTTG GACTTCTTG GCTATGCCAA	1080
	GAAGTGTAAG AGAATTGATA TTCAGTTGGA AGTGTGGAGT TGGGAAGAGT GAAGAATTGA	1140
35	CACTTGGTTC CATTAGCTTT AATGTGGGTG GTGTGGAGAG AGAGAGAAAT AGGAGAGCTT	1200
	TTGAGGGGGT AGAGTTGAGC TTTCTCAGT TGAGAAGTAG CCTTTGATAT CTTTTTTTTT	1260
40	TTTTTTTGTA CACCCATAGA ATTCCCAATT GTATAGAAGA TTGGGTGGAG TTTGTAGAGA	1320
	ATCATCTTTT GTAGTAGATT CTTTACCTTT TGGTATATCC ATTGTATACA GCCAGGCCTT	1380
	TGACTATGTT TATGAATGAA TATACATTAC TTGAAAAAAA AAGAAGTGAA GCCAGTCTGT	1440
45	TGTACCTTTG TAGACAATGT TGTGTCAGCA TCTTGATAAT TCCCTGAAAA TTGTCTCCCT	1500
	GAAGGAATAG TTTGGTTGAT ATTGATTATT TCTTGGTTTG TTTAATTCGG GTTCTTGAA	1560
50	GGCCATTTTA AATCCTTTGA CATTGTAAAA GGTGTTTACA AGTGTGGTC TGGGTTTAAA	1620
	AGCACCTCTT GTATGGTGCT TTCTGGAGTG ATCTTCTTTC CTCCAAAAGA GAAGTTGCAA	1680
	GAATCAGTGT GTGTACTTTT TTCTCTTGTA TGATCAGATC TTTTTCAT TTTTCCGTTT	1740
55	TAGTTGATTT ATCCATATAG TGAAAGTTGG TGTCATAGTT GCTGTTTGTG GACTTCCTGT	1800
	AAAAGTTTTT TGATATACTT AAAAAATTGT CACACAGAAG AAAGAGTTTT TTACCATTAC	1860

	TTAAGCTAGA TGGGACTGTT TGATTCTTAG ACCAAATAAT GAACCTTTT GTTCTCTTAA	1920
	CGTGTA CTG AAATAGTTTG GTAAAATTGT GATAGGAAAA AAGATAATTC TTGATTGCTT	1980
5	TTGGAGCATC ACTTCTAATC ATAAAAGTCT TTGCTCTCTT CAACCATGAA TGATAAATTG	2040
	GACACTTATG TGGCCCTAAG TTGCTCTCAG TAGTGGTCTT TAATTGTGGA GATATAACTA	2100
10	ATCTGATATA TGTATGTAGG GA	2122

CLAIMS

1. A method of affecting enzymatic activity in a plant (or a cell, a tissue or an organ thereof) comprising expressing in the plant (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence codes, partially or completely, for an intron of a class A potato starch branching enzyme in an antisense orientation, optionally together with a nucleotide sequence which codes, partially or completely, for an intron of a class B starch branching enzyme in an antisense or sense orientation; and wherein the nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.
2. A method according to claim 1 wherein starch branching enzyme activity is affected and/or wherein the levels of amylopectin are affected and/or the composition of starch is changed.
3. A method of affecting enzymatic activity in a starch producing organism (or a cell, a tissue or an organ thereof) comprising expressing in the starch producing organism (or a cell, a tissue or an organ thereof) a nucleotide sequence wherein the nucleotide sequence codes, partially or completely, for an intron of a class A starch branching enzyme in an antisense orientation, optionally together with a nucleotide sequence which codes, partially or completely, for an intron of a class B starch branching enzyme in an antisense or sense orientation; and wherein starch branching enzyme activity is affected and/or the levels of amylopectin are affected and/or the composition of starch is changed.
4. A method according to claim 3 wherein the nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.
5. A method according to any one of the preceding claims wherein the enzymatic activity is reduced or eliminated.

6. A method according to any one of the preceding claims wherein the nucleotide sequence codes for at least substantially all of at least one intron in an antisense orientation.

5

7. A method according to any one of the preceding claims wherein the nucleotide sequence codes for all of at least one intron in an antisense orientation.

8. A method according to any one of the preceding claims wherein the nucleotide sequence comprises the complement of SEQ. ID. No. 38, or a fragment thereof.

9. A method according to any one of the preceding claims wherein the nucleotide sequence is expressed by a promoter having a sequence shown as SEQ.I.D. No. 14 or a variant, derivative or homologue thereof.

10. An antisense sequence comprising the nucleotide sequence as defined in claim 8 or a variant, derivative or homologue thereof.

11. A promoter having a sequence shown as SEQ.I.D. No. 14, or a variant, derivative or homologue thereof.

12. A promoter according to claim 11 in combination with a gene of interest ("GOI").

25

13. A construct capable of comprising or expressing the invention according to any one of claims 10 to 12.

14. A vector comprising or expressing the invention according to any one of claims 10 to 13.

30

15. A combination of nucleotide sequences comprising a first nucleotide sequence coding for a recombinant enzyme; and a second nucleotide sequence which corresponds to an intron in antisense orientation; wherein the intron is an intron that is associated with a genomic gene encoding an enzyme corresponding to the recombinant enzyme; and wherein the second nucleotide sequence does not contain a sequence that is antisense to an exon sequence normally associated with the intron.

16. A cell, tissue or organ comprising or expressing the invention according to any one of claims 10 to 15.

10

17. A transgenic starch producing organism comprising or expressing the invention according to any one of claims 10 to 16.

18. A transgenic starch producing organism according to claim 17 wherein the organism is a plant.

15

19. A starch obtained from the invention according to any one of the preceding claims.

20

20. A nucleotide sequence that is antisense to an intron of class A SBE.

21. A method for modifying starch production in an organism, comprising transforming the organism with a transgene capable of expressing an antisense intron sequence relating to class A SBE and a transgene capable of expressing an antisense intron sequence relating to class B SBE, thereby reducing or eliminating endogenous class A and class B production, and a further sequence encoding a SBE from a heterologous source.

25

1 / 27

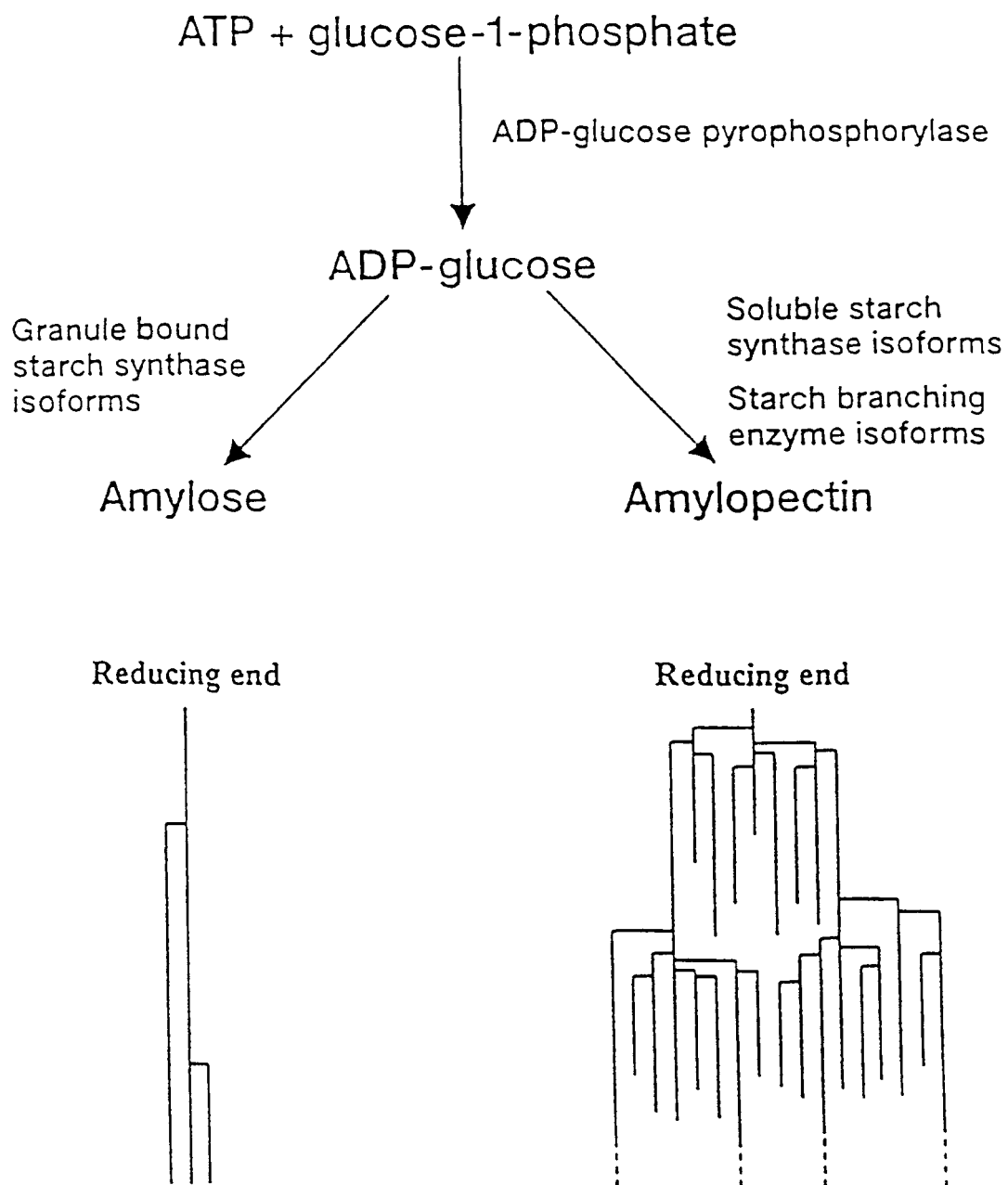
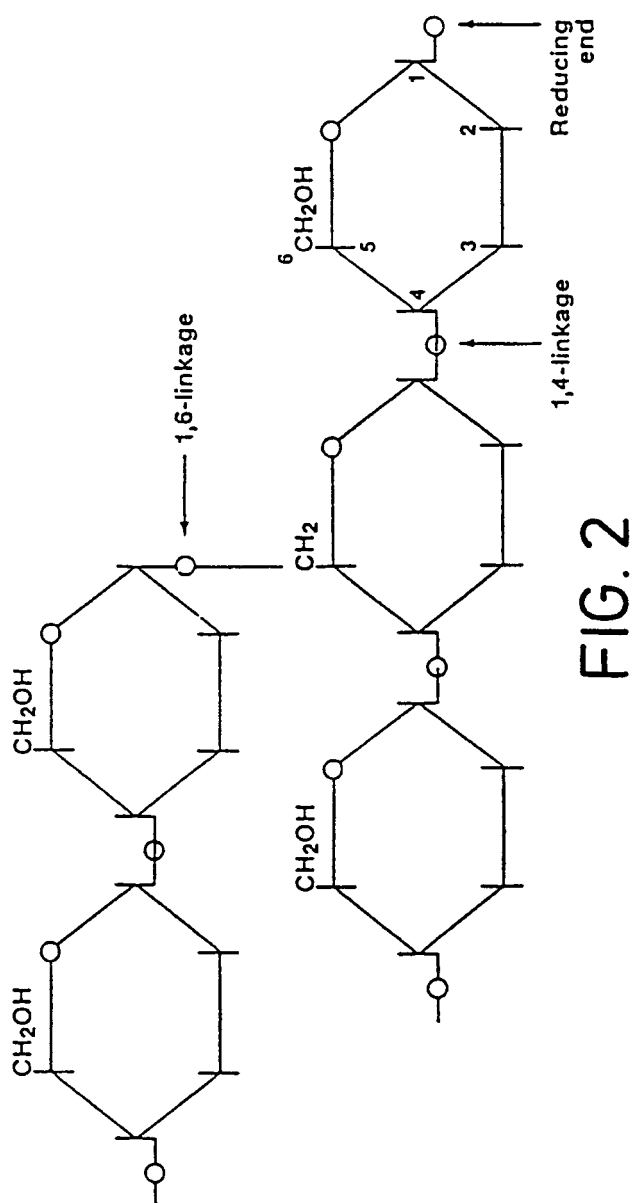


FIG. 1



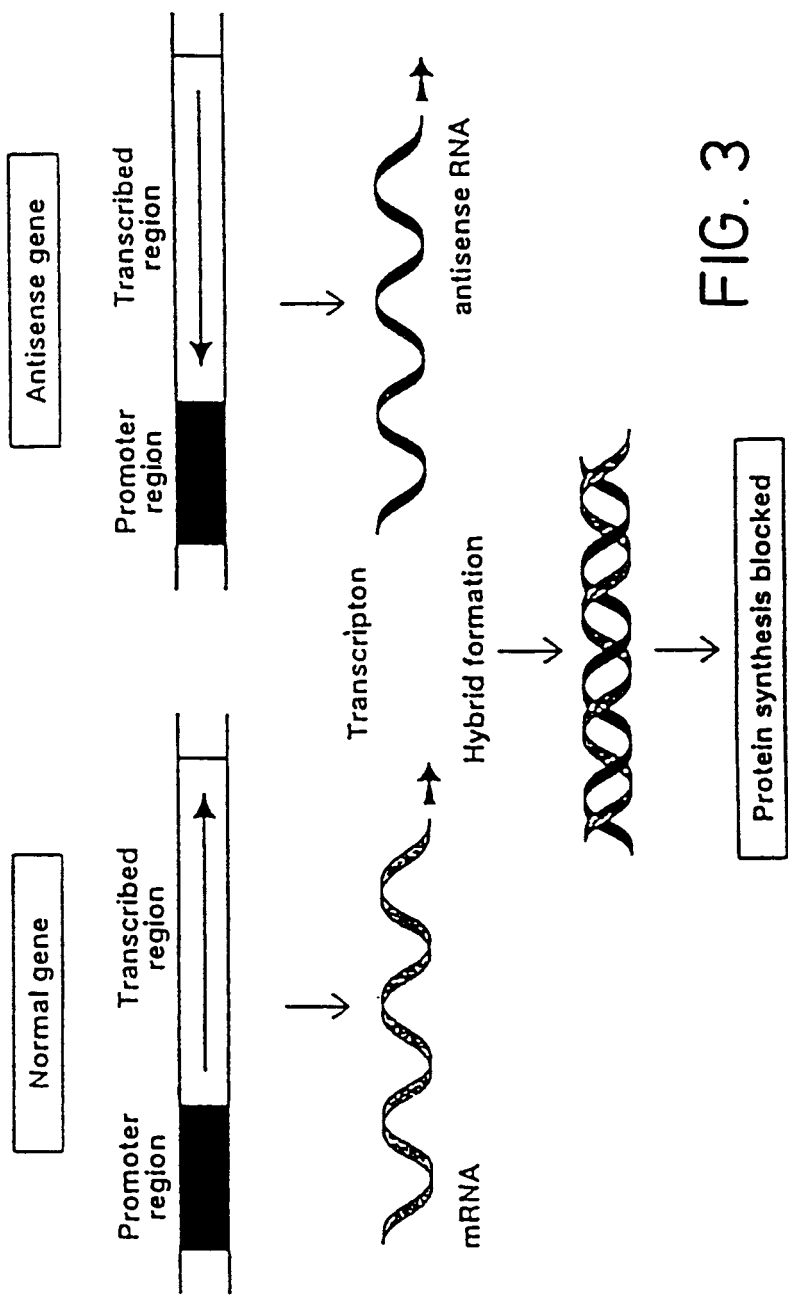


FIG. 3

4 / 27

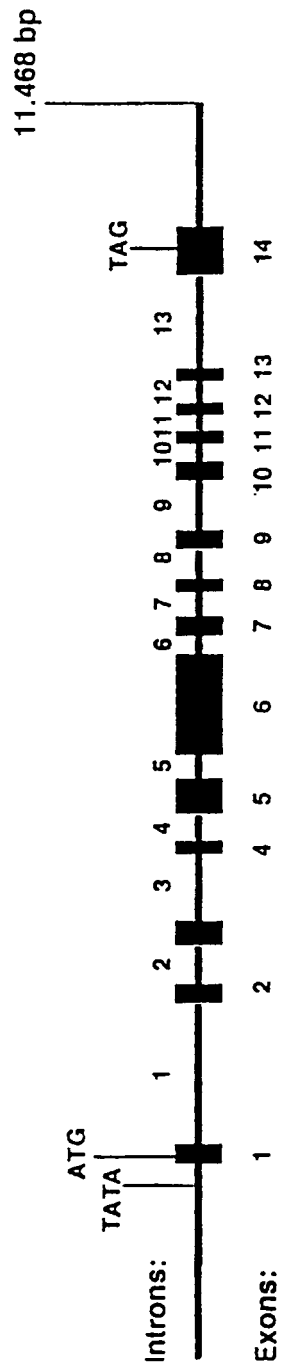


FIG. 4

5 / 27

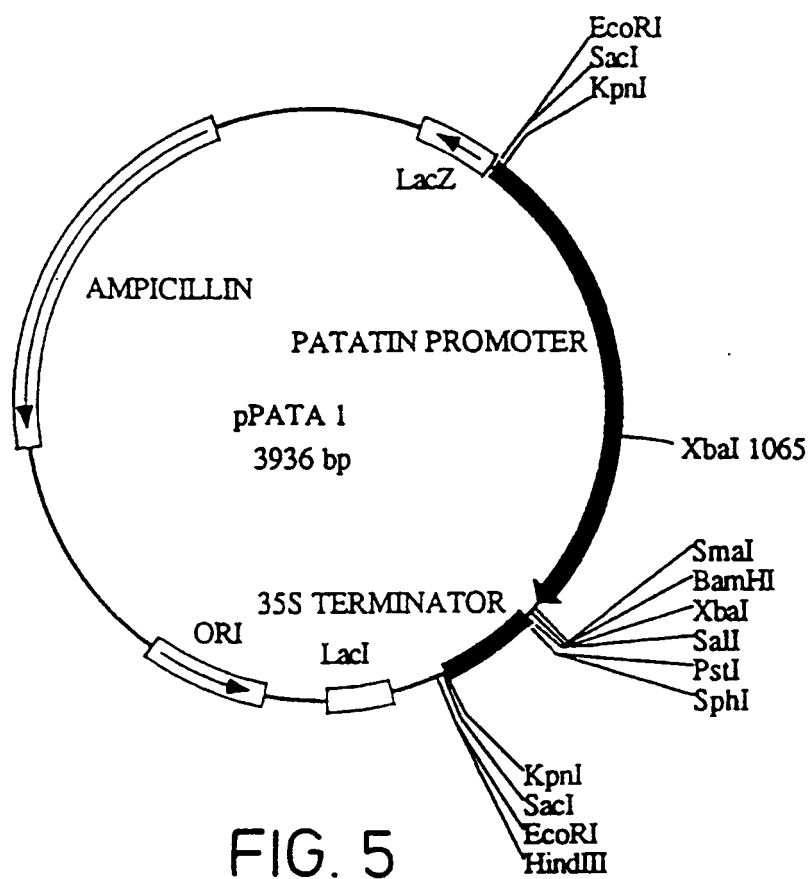
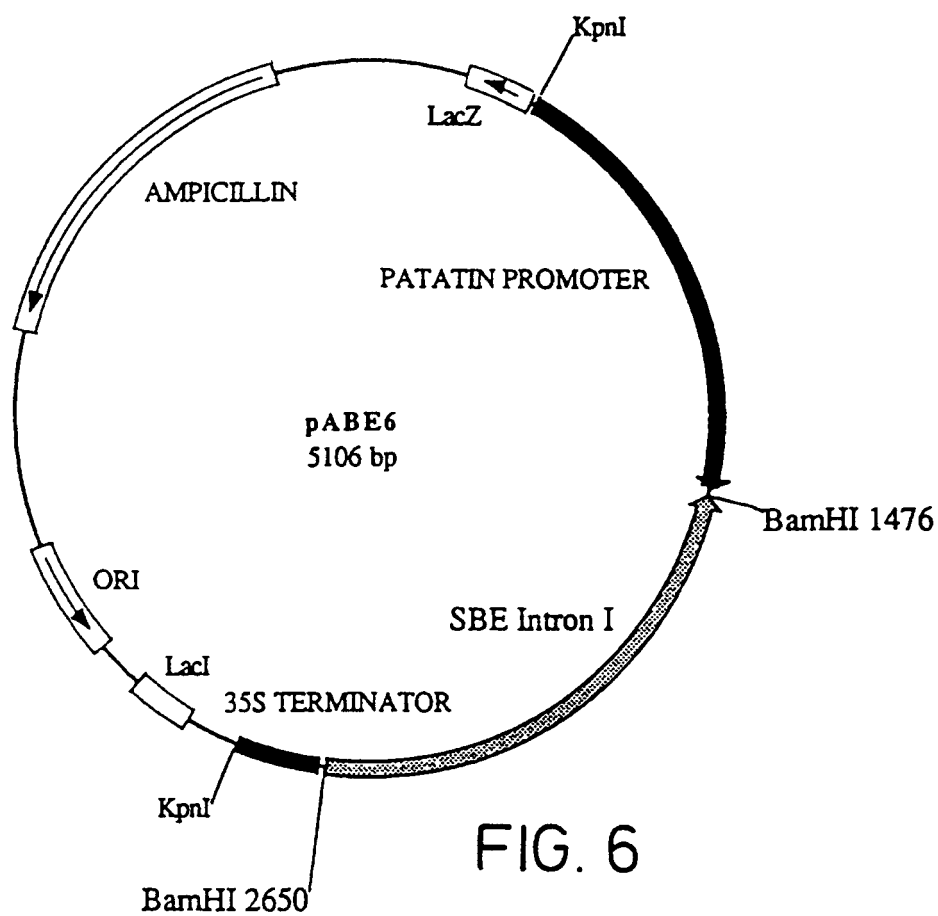


FIG. 5

6 / 27



7 / 27

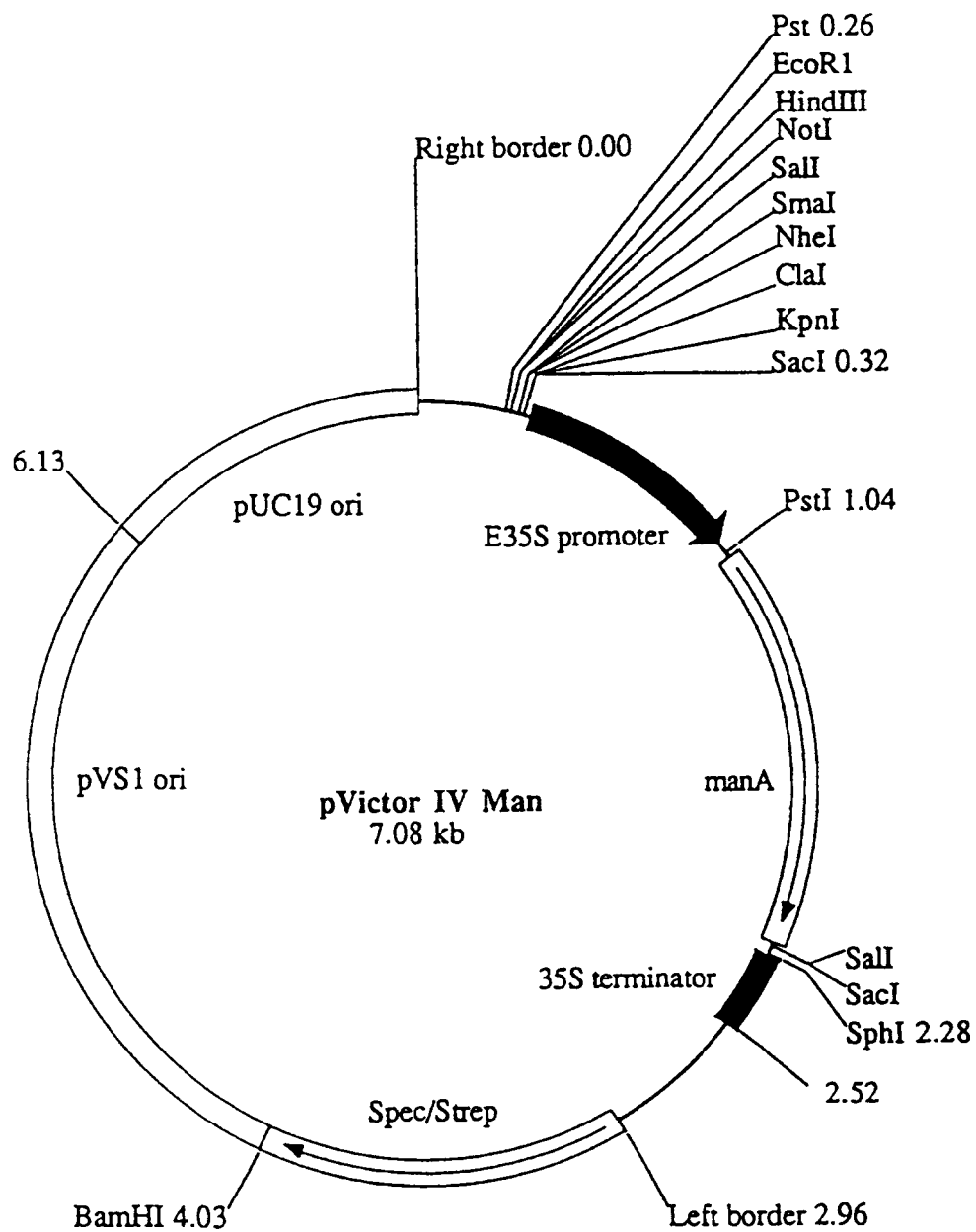


FIG. 7

8 / 27

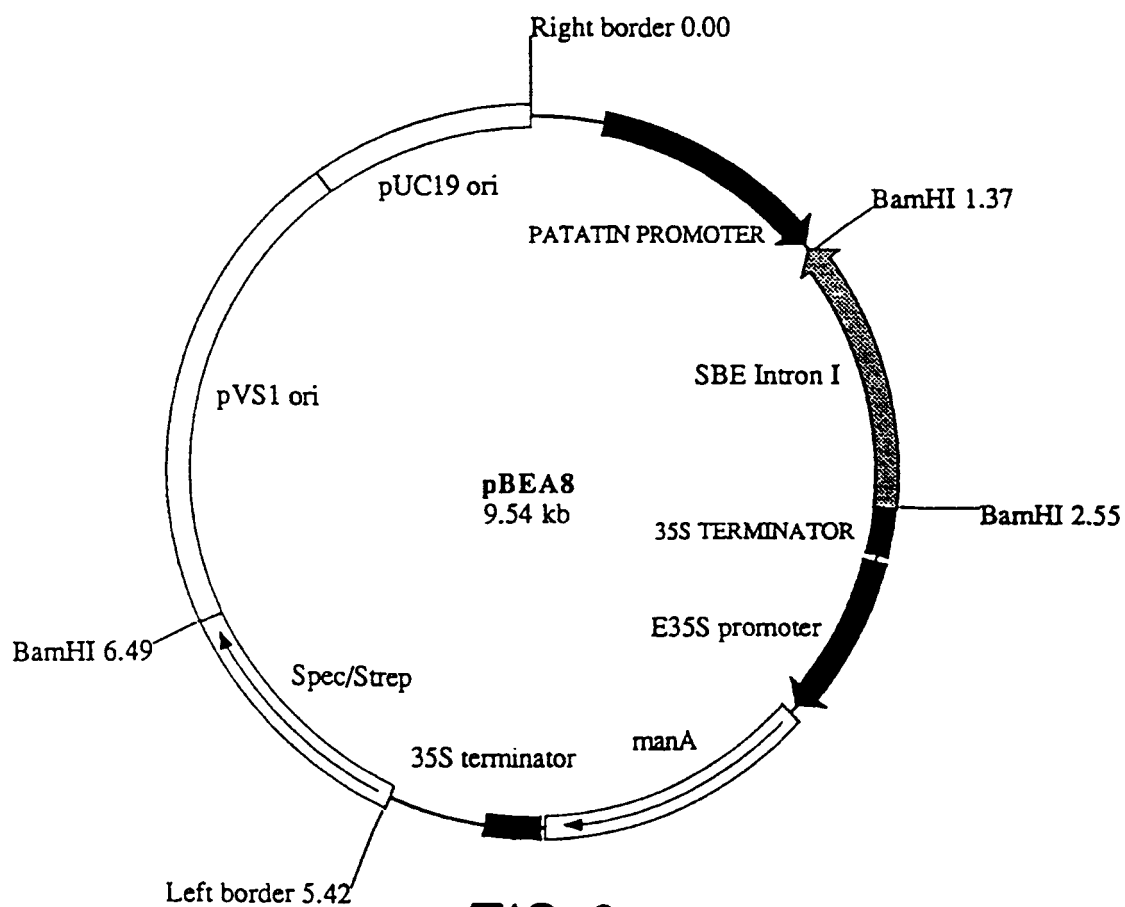


FIG. 8

9 / 27

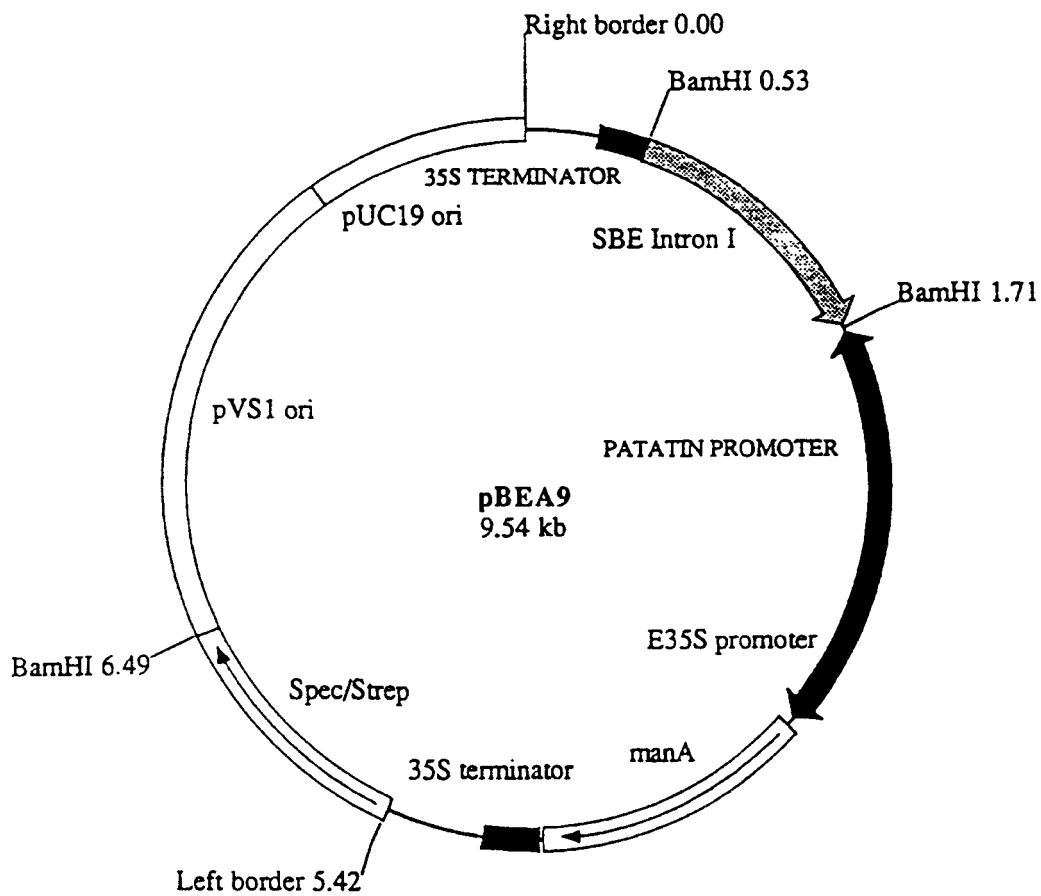


FIG. 9

10 / 27

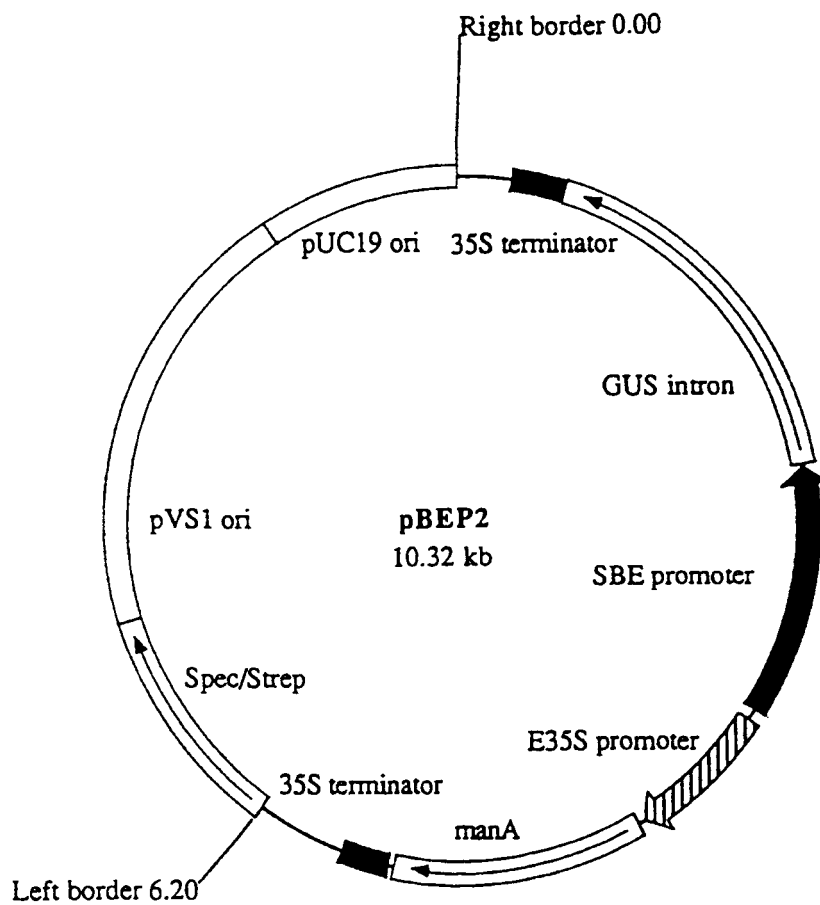


FIG. 10

11 / 27

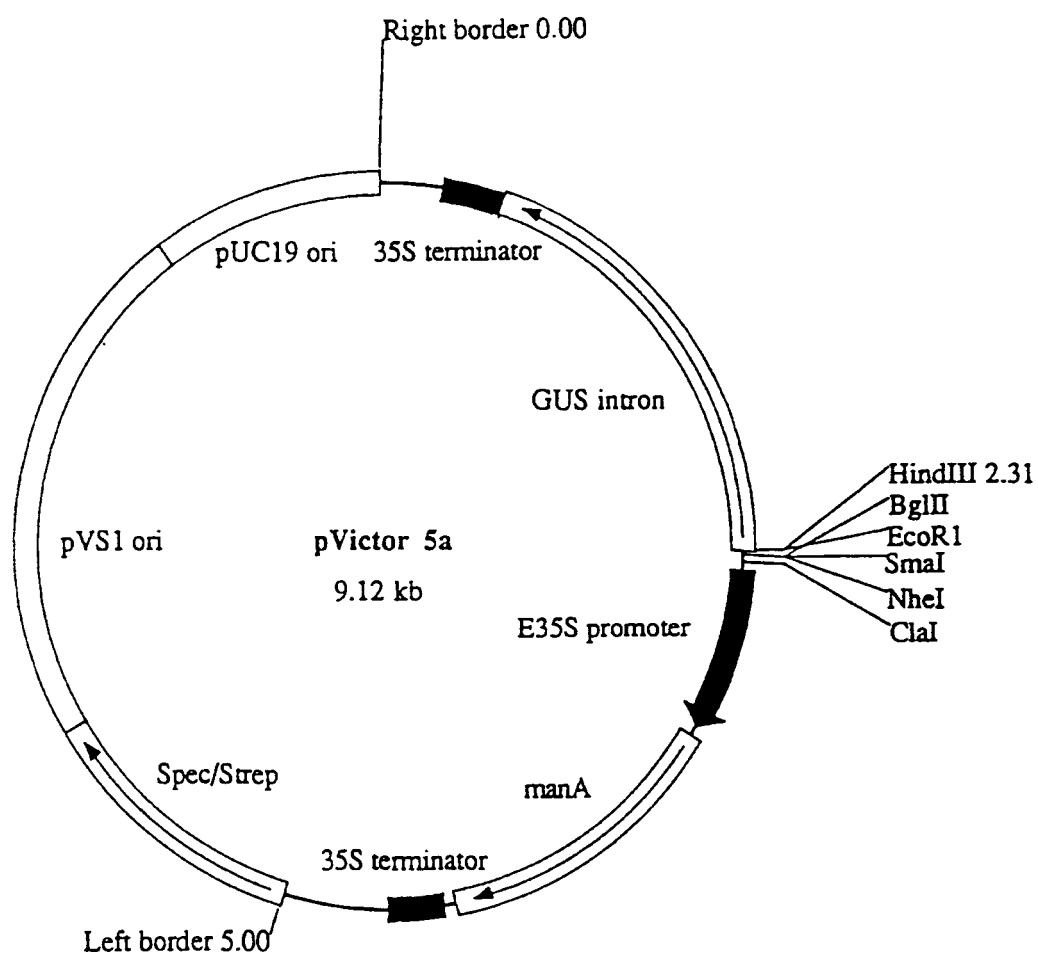


FIG. 11

12 / 27

10	20	30	40	50	60	
12345678901234567890123456789012345678901234567890						
ATCATGGCCAATTACTGGTTCAAATGCATTACTTCCTTTCAGATTCTTTCGAGTTCTCAT						60
GACCGGTCCTACTACAGACGATACTAACCCGTGGAAGTGTGCATCTGCTTCTTAGAACT						120
CTATGGCTATTTTCGTTAGCTTGGCGTCGGTTTGAACATAGTTTTTGTTCAAACTCTT						180
CATTTACAGTCAAAATGTTGTATGGTTTTTGTTCCTCAATGATGTTTACAGTGTGTG						240
TTGTCATCTGTACTTTTGCCTATTACTTGTTCCTGAGTTACATGTTAAAAAGTGTATT						300
TTGCCATATTTTGTCTCTTATTATTATTATCATACATACATTATTACAAGGAAAAGACA						360
AGTACACAGATCTTAACGTTTATGTTCAATCAACTTTTGGAGGCATTGACAGGTACCACA						420
AATTTTGAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAACATCTATTATAGATG						480
CATAAAATAGCTAATGATAGAACATTGACATTTGGCAGAGCTTAGGGTATGGTATATCC						540
AACGTTAATTTAGTAATTTTGTACGTACGTATATGAAATATTGAATTAATCACATGAA						600
CGGTGGATATTATATTATGAGTTGGCATCAGCAAAATCATTGGTGTAGTTGACTGTAGTT						660
GCAGATTTAATAATAAAATGGTAATTAACGGTCGATATTAATAAATCTCATTTCAGT						720
GGGATTAGAACTAGTTATTAAAAAATGTATACTTTAAGTGATTTGATGGCATATAATTT						780
AAAGTTTTTCATTTTCATGCTAAATTTGTTAATTATTGTAATGTAGACTGCGACTGGAATT						840
ATTATAGTGTAATTTTATGCATTCAAGTGTAAATTAAGTATTGAACCTGTCTGTTTTAG						900
AAAATACTTTTATACTTTAATATAGGATTTTGTATGCGAATTTAAATTAATCGATATTGA						960
ACACGGAATACCAAAATTAAGGATACACATGGCCTTCATATGAACCGTGAACCTTTG						1020
ATAACGTGGAAGTTCAAAGAAGGTAAAGTTAAGAATAAACTGACAAATTAATTTCTTTT						1080
ATTTGGCCCACTACTAAATTTGCTTTACTTTCTAACATGTCAAGTTGTGCCCTCTTAGTT						1140
GAATGATATTCATTTTTTCATCCATAAGTTCAATTTGATTGTCATACCACCATGATGTT						1200
CTGAAAAATGCTTGGCCATTACAAAGTTTATCTTAGTTCCTATGAACCTTTATAAGAAGC						1260
TTTAATTTGACATGTTATTTATATTAGATGATATAATCCATGACCCAATAGACAAGTGTA						1320
TTAATATTGTAACTTTGTAATTGAGTGTGTCTACATCTTATTCAATCATTTAAGGTCATT						1380
AAAATAAATTATTTTTGACATTCTAAAACCTTTAAGCAGAATAAATAGTTTATCAATTAT						1440
TAAAAACAAAAACGACTTATTTATAAATCAACAAACAATTTTAGATTGCTCCAACATAT						1500

FIG. 12

SUBSTITUTE SHEET (rule 26)

13 / 27

10	20	30	40	50	60	
12345678901234567890123456789012345678901234567890						
TTTTCCAAATTAAATGCAGAAAATGCATAATTTTATACTTGATCTTTATAGCTTATTTTT						1560
TTTAGCCTAACCAACGAATATTGTAAACTCACAACCTTGATTAAAAGGGATTACAACAA						1620
GATATATATAAGTAGTGACAAATCTTGATTTTAAATATTTTAATTTGGAGGTCAAAATTT						1680
TACCATAATCATTTGTATTTATAAATTTTAAATATCTTATTTATACATATCTAGTA						1740
AACTTTTAAATATACGTATATACAAAATATAAAATTATTGGCGTTCATATTAGGTCAATA						1800
AATCCTTAACATATCTGCCTTACCACTAGGAGAAAGTAAAAAACTCTTTACCAAAAATA						1860
CATGTATTATGTATACAAAAGTCGATTAGATTACCTAAATAGAAATTGTATAACGAGTA						1920
AGTAAGTAGAAATATAAAAAAACTACAATACTAAAAAAAATATGTTTTACTTCAATTTTCG						1980
AAACTAATGGGGTCTGAGTGAAATATTCAGAAAGGGGAGGACTAACAAAAGGGTCATAAT						2040
GTTTTTTTATATAAAAAGCCACTAAAATGAGGAAATCAAGAATCAGAACATACAAGAAGGCA						2100
GCAGCTGAAGCAAAGTACCATAATTTAATCAATGGAAATTAATTTCAAAGTTTTATCAAA						2160
ACCCATTCGAGGATCTTTCCATCTTTCTCACCTAAAGTTTCTTCAGGGgtaatttttac						2220
P I R G S F P S F S P K V S S G						
taatttcacgttaatttcaattattttagcctttgcatttcattttccaatatatctgg						2280
atcatctccttagttttttattttattttttataatatcaaatatggaagaaaaatgaca						2340
cttgtagagccatagttaagtatcatgtgacaaatttgcaaggtgggtgagtgtataaaa						2400
ttcaaaaattgagagatggaggggggggtaggggbaragacaatattagaaagagtgttc						2460
taggaggttatggaggacacggatgaggggtagaagggttagttaggtatttgagtgttgt						2520
ctggccttatcctttcactactagtagtcgtggaattatgtggtagtttctgttttgta						2580
tttgatccttggtatttctattttctgtttctgtacttcgattattgtattatatatctt						2640
gtcgtagttattgttcctcggaagaatgctctagcatgcttcctttagtgttttatcat						2700
gccttctttatattcgcgttgctttgaaatgcttttacttttagccgaggggtctattagaa						2760
acaatctctctatctcgtaaggtaggggtaaagtcctcaccacactccacttggtgggatt						2820
acattgtgtttgttggtgttaaataattatgtatacataataagtggattttttacaaca						2880
caaatacatggtcaagggcaaagttctgaacacataaagggttcattatatgtccaggga						2940
tatgataaaaattgtttctttgtgaaagttatataagatttggttatggccttttgctggaa						3000

FIG. 12 CONTINUED

SUBSTITUTE SHEET (rule 26)

14 / 27

10	20	30	40	50	60	
12345678901234567890123456789012345678901234567890						
acataataagttataatgctgagatagctactgaagtttggtttttctagccttttaaat						3060
gtaccaataatagattccgtatcgaacgagtatggttttgattacctggatcatgatgtttc						3120
tattttttacatttttttggtgttgaaactgcaattgaaaatggtgtatcctatgagacgg						3180
atagttgagaatgtgttctttgtatggaccttgagaagctcaaacgctactccaataatt						3240
tctatgaattcaaattcagtttatggctaccagtcagtcagaaattaggatagctgca						3300
tatacttgttcaattatactgtaaaatttcttaagttctcaagatatccatgtaacctcg						3360
agaatttctttgacagGCTTCTAGAAATAAGATATGTTTTCTTCTCAACATAGTACTGG						3420
ACTGAAGTTTGGATCTCAGGAACGGTCTTGGGATATTTCTTCCACCCCAAAATCAAGAGT						3480
TAGAAAAGATGAAAGGgtatggtttgataatttatatgggtgcatggatagtatataaata						3540
R K D E R						
gttggaacttctggactggtgctcatggcatatttgatctgtgcaccgtgtggagatg						3600
tcaaacatgtgttacttcgttccgccaatttataataaccttaacttgggaagacagctc						3660
tttactcctgtgggcattttgttatttgaattacaatctttatgagcatggtgttttcaca						3720
ttatcaacttctttcatgtggtatataacagtttttagctccgttaataacctttcttctt						3780
tttgatataaaactaactgtggtgcatgtgcttgcbkkkATGAAGCACAGTTCAGCTATTTT						3840
CGCTGTTTTGACCGATGACGACAATTCGACAATGGCACCCCTAGAGGAAGATGTCAAGAC						3900
ACACAGAATGAAGAGATATGTGGATCAGAAAATGCTCATTGAAAAATATGAGGGACCCCT						3960
TGAAAATATTGGCCTCCTAAATTTGGATCCAACCTTTGGAACCTTATCTAGATCACTTCAG						
ACACAGAATGAAGAGATATGTGGATCAGAAAATGCTCATTGAAAAATATGAGGGACCCCT						4020
TGAGGAATTTGCTCAAGgtaacagccaaaagttgtgcttttaggcagtttgaccttatttt						4080
E E F A Q G						
ggaagatgaattgtttataacctactttgacttttgctagagaattttgcataccggggagt						4140
aagtagtggctccatttaggtggcacctggccatttttttgatcttttaaaaagctgttt						4200
gattgggtcttcaaaaaagtagacaaggttttttgagaagtgacacacccccggagtgtc						4260
agtggcaaagcaaagattttcactaaggagattcaaaatataaaaaaagtatagacataa						4320
agaagctgaggggattcaacatgtactatacaagcatcaaatatagtcttaaagcaattt						4380
tgtagaaataaagaaagtcttcttctgtgtgcttcacaatttcttctattatcatgagt						4440
tactctttctgttcgaaatagcttcttcttaattataaattcatgatacttttgttgagatt						4500

FIG. 12 CONTINUED

SUBSTITUTE SHEET (rule 26)

15 / 27

10	20	30	40	50	60	
123456789012345678901234567890123456789012345678901234567890						
tagcagtttttttctgtgtaaaactgctctctttttttgcagGTTATTTAAAATTTGGATT						4560
				Y L K F G F		
CAACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTGCTCagtaggtcct						4620
N R E D G C I V Y R E W A P A A Q						
cgtctactacaaaatagtagtttccatcatcataacagattttcctattaaagcatgatg						4680
ttgcagcatcattggcctttcttacatgttctaattgctattaagggttatgcttctaatta						4740
actcatccacaatgcagGGAAGCAGAAGTTATTGGCGATTTCATGGATGGAACGGTTCT						4800
				E A E V I G D F N G W N G S		
AACCACATGATGGAGAAGGACCAGTTTGGTGTTTGGAGTATTAGAATTCCTGATGTTGAC						4860
N H M M E K D Q F G V W S I R I P D V D						
AGTAAGCCAGTCATTCCACACAACCTCCAGAGTTAAGTTTCGTTTCAAACATGGTAATGGA						4920
S K P V I P H N S R V K F R F K H G N G						
GTGTGGGTAGATCGTATCCCTGCTTGGATAAAGTATGCCACTGCAGACGCCACAAAGTTT						4980
V W V D R I P A W I K Y A T A D A T K F						
GCAGCACCATATGATGGTGTCTACTGGGACCCACCACCTTCAGAAAGgttttgttattca						5040
A A P Y D G V Y W D P P P S E R						
taccttgaagctgaattttgaacaccatcatcacaggcatttcgattcatgttcttacta						5100
gtcttgttatgtaagacattttgaaatgcaaaaagttaaaataaattgtgtcttttactaatt						5160
tggaacttgatcccatactctttcccttaacaaaatgagtcattctataaagtgttgaga						5220
acttactacttcagcaattaaacagGTACCACTTCAAATACCCCTCGCCCTCCCAAACCCC						5280
				Y H F K Y P R P P K P R		
GAGCCCCACGAATCTATGAAGCACATGTGCGCATGAGCAGCTCTGAGCCACGTGTAAATT						5340
A P R I Y E A H V G M S S S E P R V N S						
CGTATCGTGAGTTTGCAGATGATGTTTTACCTCGGATTAAGGCAAATAACTATAATACTG						5400
Y R E F A D D V L P R I K A N N Y N T V						
TCCAGTTGATGGCCATAATGGAACATTCTTACTATGGATCATTGGATATCATGTTACAA						5460
Q L M A I M E H S Y Y G S F G Y H V T N						
ACTTTTTTGTGTGAGCAGTAGATATGGAACCCGAGGACCTAAAGTATCTGATAGATA						5520
F F A V S S R Y G N P E D L K Y L I D K						
AAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACAGTCATGCAAGCAATA						5580
A H S L G L Q V L V D V V H S H A S N N						
ATGTCATGATGGCCTCAATGGCTTTGATATTGGCCAAGGTTCTCAAGAATCCTACTTTC						5640
V T D G L N G F D I G Q G S Q E S Y F H						
ATGCTGGAGAGCGAGGGTACCATAAGTTGTGGGATAGCAGGCTGTTCAACTATGCCAATT						5700
A G E R G Y H K L W D S R L F N Y A N W						
GGGAGGTTCTTCGTTTCTTTTCCAACCTTGAGGTGGTGGCTAGAAGAGTATAACTTTG						5760
E V L R F L L S N L R W W L E E Y N F D						
ACGGATTTTCGATTTGATGGAATAACTTCTATGCTGTATGTTTCATCATGGAATCAATATGG						5820
G F R F D G I T S M L Y V H H G I N M G						
GATTTACAGGAACTATAATGAGTATTTACGCGAGGCTACAGATGTTGATGCTGTGGTCT						5880
F T G N Y N E Y F S E A T D V D A V V Y						
ATTTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCAGATGCAACTGTTATTGCCG						5940
L M L A N N L I H K I F P D A T V I A E						
AAGATGTTTCTGGTATGCCGGGCCTTGGCCGGCCTGTTTCTGAGGGAGGAATTGGTTTGTG						6000
D V S G M P G L G R P V S E G G I G F V						

FIG. 12 CONTINUED

SUBSTITUTE SHEET (rule 26)

16 / 27

10	20	30	40	50	60	
12345678901234567890123456789012345678901234567890						
TTTACCGCCTGGCAATGGCAATCCCAGATAAGTGGATAGATTATTTAAAGAATAAGAAATG						6060
Y R L A M A I P D K W I D Y L K N K N D						
ATGAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGA						6120
E D W S M K E V T S S L T N R R Y T E K						
AGTGTATAGCATATGCGGAGACCCATGATCAGgtatttttaaatttttctacaactaaa						6180
C I A Y A E T H D Q						
taatttctcagaacaattgttagatagaatccaaatatatacgtcctgaaagtataaaaagt						6240
acttatttttcgccatgggccttcagaatatgttagccgctgaatatcatgataagttat						6300
ttatccagtgacatttttatgttcactcctattatgtctgctggatacagTCTATTGTG						6360
				S I V G		
GTGACAAGACCATTCGATTCTCTCTAATGGACAAAGAGATGTATTCTGGCATGTCTTGCT						6420
D K T I A F L L M D K E M Y S G M S C L						
TGACAGATGCTTCTCCTGTTGTTGATCGAGGAATTGCGCTTCACAAGgtttgtctgtttc						6480
T D A S P V V D R G I A L H K						
tattgcatttttaagggttcatatagggttagccacggaaaatctcactcctttgtgaggttaac						6540
cagggttctgatggattattcaattttctcgtttatcatttgtttattccttttcatgcat						6600
tgtgtttctttttcaatatccctcttatttggaggtaatttttctcatctattcactttt						6660
agcttcttaaccacagATGATCCATTTTTTCACAATGGCCTTGGGAGGAGAGGGGTACCTC						6720
M I H F F T M A L G G E G Y L						
AATTTCATGGGTAACGAGgtatgtcttacatcttttagatattttgtgataattacaatta						6780
N F M G N E						
gtttggcttacttgaacaagattcattcctcaaaatgacctgaactgttgaacatcaaag						6840
gggttgaacatagaggaaaacaacatgatgaatgtttccattgtctagggatttctatt						6900
atgttgctgagaacaaatgtcatcttaaaaaaacattgtttactttttttagtataga						6960
agattactgtatagagtttgcaagtgtgtctgttttggagtaattgtgaaatgtttgatg						7020
aacttgtacagTTTGGCCATCCTGAGTGGATTGACTTCCCTAGAGAGGGCAATAATTGGA						7080
F G H P E W I D F P R E G N N W S						
GTTATGACAAATGTAGACGCCAGTGAACCTCGCGGATAGCGAACACTTGAGATACAAGg						7140
Y D K C R R Q W N L A D S E H L R Y K						
ttcaagtattttgaatcgagcttgttaataatctagtaatttttagattgcttacttg						7200
gaagtctacttgggttctggggatgatagctcatttcatttcttacttattttccaac						7260
cgaatttctgatttttgtttcgagatccaagtattagattcatttacacttattaccgcc						7320
tcatttctaccactaaggccttgatgagcagcttaagttgattccttgaagctatagttt						7380
caggctaccaatccacagcctgctatatttgttggatacttaccttttctttacaatgaa						7440
gtgatactaattgaaatgggtctaaatctgatatctatatttctccgtctttcctccccct						7500

FIG. 12 CONTINUED

SUBSTITUTE SHEET (rule 26)

17 / 27

10	20	30	40	50	60	
123456789012345678901234567890123456789012345678901234567890						
catgatgaaatgcagTTTATGAATGCATTTGATAGAGCTATGAATTCGCTCGATGAAAAG						7560
	F M N A F D R A M N S L D E K					
TTCTCATTCCTCGCATCAGGAAAACAGATAGTAAGCAGCATGGATGATGATAATAAGgta						7620
F S F L A S G K Q I V S S M D D D N K						
aaatcatcttaaagttgaaagtgttgggtttatgaagtgccttaattctatccaaggacaa						7680
gtagaaacctttttaccttccatttcttgatgatggatttcatattatccaatag						7740
ctgggtcaaattcggtaaatagctgtactgatttagttacttccatttgcagGTTGTTGTGTT				V V V F		7800
TGAACGTGGTGACCTGGTATTTGTATTCAACTTCCACCCAAAGAACACATACGAAGGgta						7860
E R G D L V F V F N F H P K N T Y E G						
tatatgttttacttatccatgaaattattgctctgcttgttttaagtactgaacaagt						7920
tttatggagaagtaactgaaacaaatcattttcacattgtctaatttaactcttttttct						7980
gatcctcgcatgacgaaaacagGTATAAAGTTGGATGTGACTTGCCAGGGAAGTACAGAG						8040
	Y K V G C D L P G K Y R V					
TTGCACTGGACAGTGTATGCTTGGGAATTTGGTGGCCATGGAAGAgtaaggatttgccttga						8100
A L D S D A W E F G G H G R						
ataacttttgataataagataacagatgtagggtagatttctctcaccaaaaagaactgt						8160
aattgtctcatccatcttttagttgtataagatatccgactgtctgagttcgggaagtgttt						8220
gagcctcctgccctccccctgcgttgttttagctaattcaaaaaggagaaaactgtttatt						8280
gatgatctttgtcttcatgctgacatacaatctgttctcatgacagACTGGTCATGATGT				T G H D V		8340
TGACCATTTCACATCACCAGAAGGAATACCTGGAGTTCAGAAACAAATTTCAATGGTCG						8400
D H F T S P E G I P G V P E T N F N G R						
TCCAAATTCCTTCAAAGTGCTGTCTCCTGCGCGAACATGTGTGgtacagttcttgccgtg						8460
P N S F K V L S P A R T C V						
tgacctccctttttattgtgggtttgttcatagttatttgaatgcatagaagttaacta						8520
ttgattaccgccacaatcgccagtttaagtcctctgaactactaatttgaaaggtaggaat						8580
agccgttaataaggcttacttttggcatcttactgttacaaaacaaaaggatgcaaaaaa						8640
attcttctctatcctctttttccctaaaccagtgcagtagcttgacctgcataaaactt						8700
aggtaaatgatcaaaaatgaagttgatgggaacttaaaacggcctgaagtaagctagg						8760
aatagtcataataatgtccacctttgggtgtctgcgctaacaacaacaacatacctcgt						8820
gtagtcacacaaagtgggtttcagggggagggtagagtgtatgcaaaacttactcctatct						8880
cagaggtagagaggattttttcaatagacccttggtcgaagaaaaaagtccaaaaagaa						8940
gtaacagaagtgaaagcaacatgtgtagctaagcgacccaacttgtttgggactgaagt						9000

FIG. 12 CONTINUED

SUBSTITUTE SHEET (rule 26)

SUBSTITUTE SHEET (rule 26)

19 / 27

10	20	30	40	50	60	
12345678901234567890123456789012345678901234567890						
TCGGGTATCAACGATGAAATGGACCAGTTGGATCGACTGCCTGCACAACGTTAGGTATGC						10560
CAAAAAAAGAACACGATCCTTTGCACCCGTTTCGATGATTATCAGTATGTTACAAAAA						10620
AACCTTAAGTTCATCCAGTGTAACAAGCCCCAACATCTGCCCCAAGTAACAAAAACAA						10680
CCAATTTATCTTATTCTTATCTGCCACAAAATAATCGGTTTCACACTATTCTCTTGTAT						10740
ACAAAATTGACAAGTAGGAAGGAGAGGAGTCATCCAAATAAACGGTGCACGTTCTTTGAG						10800
AAAAGTCTTATTTTTCGTAAGATCCAATTTCAACAACTTTTCTTCAAGTCAAAATTCCT						10860
GATAGTGTATCTCCTCTCGACGACCTCTTGCAATTGAACGATCTCCGCTTATCATGAAAAG						10920
TTGCTTGGATAACAAGTATTGCAAGGGGGGACAGTAGCTATTAAGTTAGTCGGCCCAAG						10980
GAAATGGAGGAGTGATAGTCTCGAATATTATTACCTCTTTAGCATTACCCGGTCTGGCT						11040
TTAAGGAGTTACGTCTTTTACGCTCGCCAATTTCTTTTTTTAGAAATGGTTGGTGTCAAAA						11100
TCGCGAGTTGTGGAAGGTTCAAGTTACTCGATTCTGTGATTTTCAAGTATGAGTGGTGAGA						11160
GAGATTCGATATTTTCACGAGGTGTATTGAGGTCTAGTAGAACGAAGGGTGTCACTAAT						11220
GAAAGTTTCAAGAGTTCATCATCATCTTCTCTAGTAGATTTTCGCTTTCAAATGAGTAT						11280
GAAAATCTTCCTCTTTTCTATTGATTTTCTTCATTGTTTCTTCATTGTTGTGGTTGTT						11340
ATTGAAAAGAAAGAAAATTTATAACAGAAAAAGATGTCAAAAAAAGGTAAAATGAAAGA						11400
GTATCATATACTTAAAGAGTTGCGTAGAGATAAGTCAAAAGAAACAGAATTATAGTAATT						11460
TCAGCTAAGTTAGAATTC						11478

FIG. 12 CONTINUED

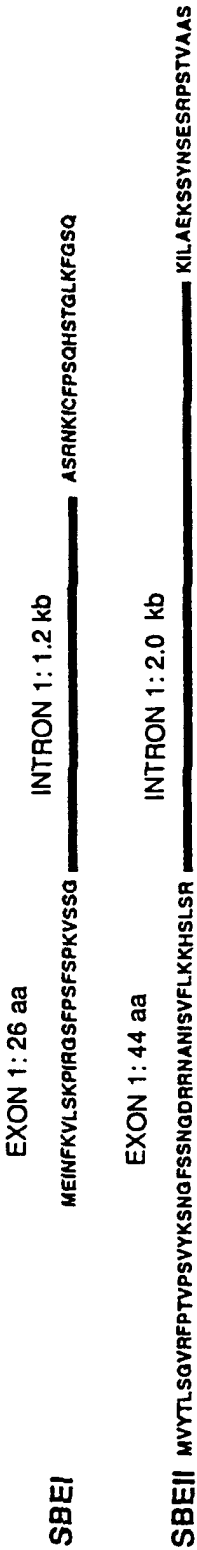


FIG. 13

21 / 27

10	20	30	40	50	60
123456789012345678901234567890123456789012345678901234567890					
<hr/>					
GTATACTCTCTGGAGTTCGTTTTCTACTGTTCCATCAGTGTACAAATCTAATGGATT					
Y T L S G V R F P T V P S V Y K S N G F					
SspI					
BsmI					
CAGCAGTAATGGTGATCGGAGGAATGCTAATATTCTGTATTCTTGAAAAACACTCTCT					
S S N G D R R N A N I S V F L K K H S L					
BsaAI					
TTCACgtatgtctcactgtgtttgtggctgtgtgtgttttttctctgtctttttgtgtt					
S R					
Bsp1286I					
BanII					
ttgtgtaattggggctctttaaagttggtattgtgtatacccttttgagtatagtctttg					
aggaagcaaatgatgaatcttgattgacattagtaagggttgtaacttttgaagtttg					
gttaggtgtaattgagtttggtctgtgtctgtgtgtcgaggtatttttttggtttgt					
gttattggggatcttaaagttggtattgtgtatacccttttgagtatagtctttgagga					
agcaaaaatgatgaatcttgattggcattagtaaagggtgtagcttttgaagtgtggtt					
agggtgtaattgagtttggtctgtgtctgtgtgttttggaaatcctgatgtgtgtcaagt					

FIG. 14

SUBSTITUTE SHEET (rule 26)

22 / 27

10	20	30	40	50	60
123456789012345678901234567890123456789012345678901234567890					
cctgatatgggtcgaggttctttctttggtttgtgtaattgggggttcttaaagttggt					600
				ClaI BspDI	
attatgtacctttttaagaatagtgtctgagaaagcaaaatcgatgaattttgattgaca					660
gcatattctttgagaaagcaaaaaatggtgagttttcatggagaaacttgattgacatta					720
ctaaaggtagcaactttttcaactcctgatatgggtcaagggtctttgtttggtttgtgt					780
aatttgggggttctttgaagttttgagaaagaaaaattatgatttttcatggagaaatttg					840
	AseI			PvuII NspBII	
atttacattaataaaggtagtagctttttaagtggtgagctgtaatgagttcagctt					900
	BspI286I BanII ApaI NdeI				
ggtttaaggggcccctacatatggtgctttctggtgagatatttggtgctccaccatac					960
gagttataagaatcatagtgttaggatctttttctttttttttcatttttcacttgac					1020
tagctactagaggagtgatcttgacggcggaatcttagaaaggggaagggtgtttgca					1080

FIG. 14 CONTINUED

SUBSTITUTE SHEET (rule 26)

23 / 27

	10	20	30	40	50	60	
123456789012345678901234567890123456789012345678901234567890							
		Esp3I		BsaBI			
tcaactggtgttatatgtgcaaggagacgggagatgatgttagatcatcttctcttcatt		▼		▼			1140
gtggtcctttccatgaggttatgatgtgatatgtttgaatggtttggtacttcttggtat							1200
					EarI		
gccagaactgtgaaagaattgatattcagttggaagtgtggagtgggaagagtggaaga					▼		1260
attgacacttgggtccattagctttaatgtgggtggtgtggagagagagagaaaataggag							1320
						EcoRV	
agcttttgagggggtagagttgagctttcctcagttgagaagtagcctttgatatactttt						▼	1380
		EcoRI	MunI				
ttttttttttttgtacaccatagaattcccattgtatagaagattgggtggagtttgt		▼	▼				1440
agagaatcatctttttagtagattcttttaccttttggatatatccattgtatacacgcag							1500
	StuI						
gcctttgactatgtttatgaatgaatatacattactgaaaaaaaaagaagtgaagccag	▼						1560
tctgttgtacctttgtagacaatgttgtgcagcatcttgataattccctgaaaaattgtc							1620

FIG. 14 CONTINUED

24 / 27

10	20	30	40	50	60
123456789012345678901234567890123456789012345678901234567890					
<hr/>					
tccctgaaggaatagtttggttgatattgattatttcttggtttgtttaattcgggtgttc					
1680					
ttgaaggccattttaaactcctttgacattgttaaagggtgtttacaagtgttggtctgggt					
1740					
ttaaaagcacctcttgatggtgctttctggagtgatctttcttctcctccaaaagagaagt					
1800					
tgcaagaatcagtggtgtacttttttctcttgatgatcagatctttttcaatttttc					
1860					
cgtttttagttgatttatccatatagtgaagttggtgtcatagttgctgtttgtggactt					
1920					
cctgtaaaagtttttgatataacttaaaaaattgtcacacagaagaagagttttttacc					
1980					
attacttaagctagatgggactgtttgattccttagaccaataatgaacctttttgttct					
2040					
cttaacgtgtacttgaaatagtttggtaaaattgtgataggaaaaaagataattcttgat					
2100					
tgcttttgagcatcacttctaatacataaaagtctttgctctcttcaaccatgaatgata					
2160					

FIG. 14 CONTINUED

SUBSTITUTE SHEET (rule 26)

25 / 27

10	20	30	40	50	60
123456789012345678901234567890123456789012345678901234567890					

aattggacacttatgtggccctaagttgctctcagtagtggtctttaattgtggagatat 2220

aactaatctgatatatgtatgtagGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCCG 2280
BglII BbsI
K I L A E K S S Y N S E

AATCCCGACCTTCTACAGTTGCAGCATCG 2309
SfcI
S R P S T V A A S

FIG. 14 CONTINUED

26 / 27

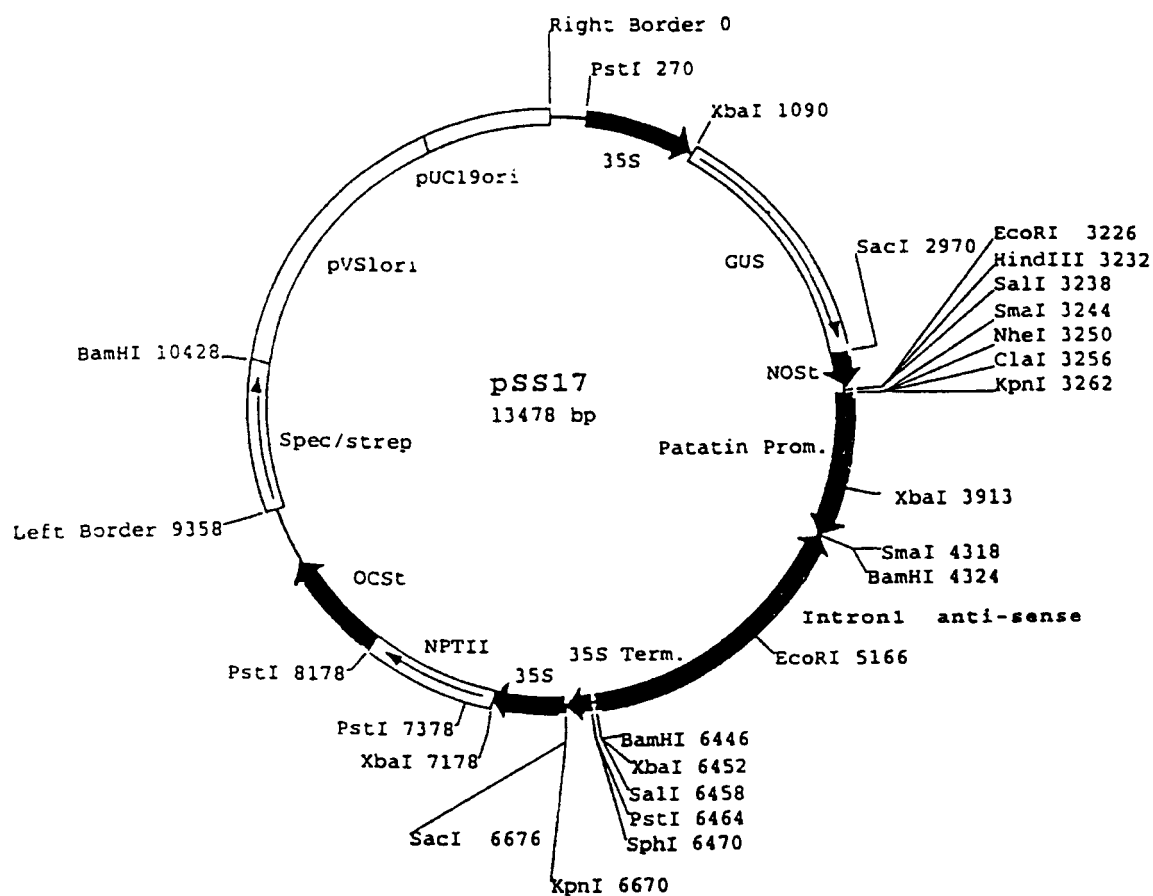


FIG. 15

27 / 27

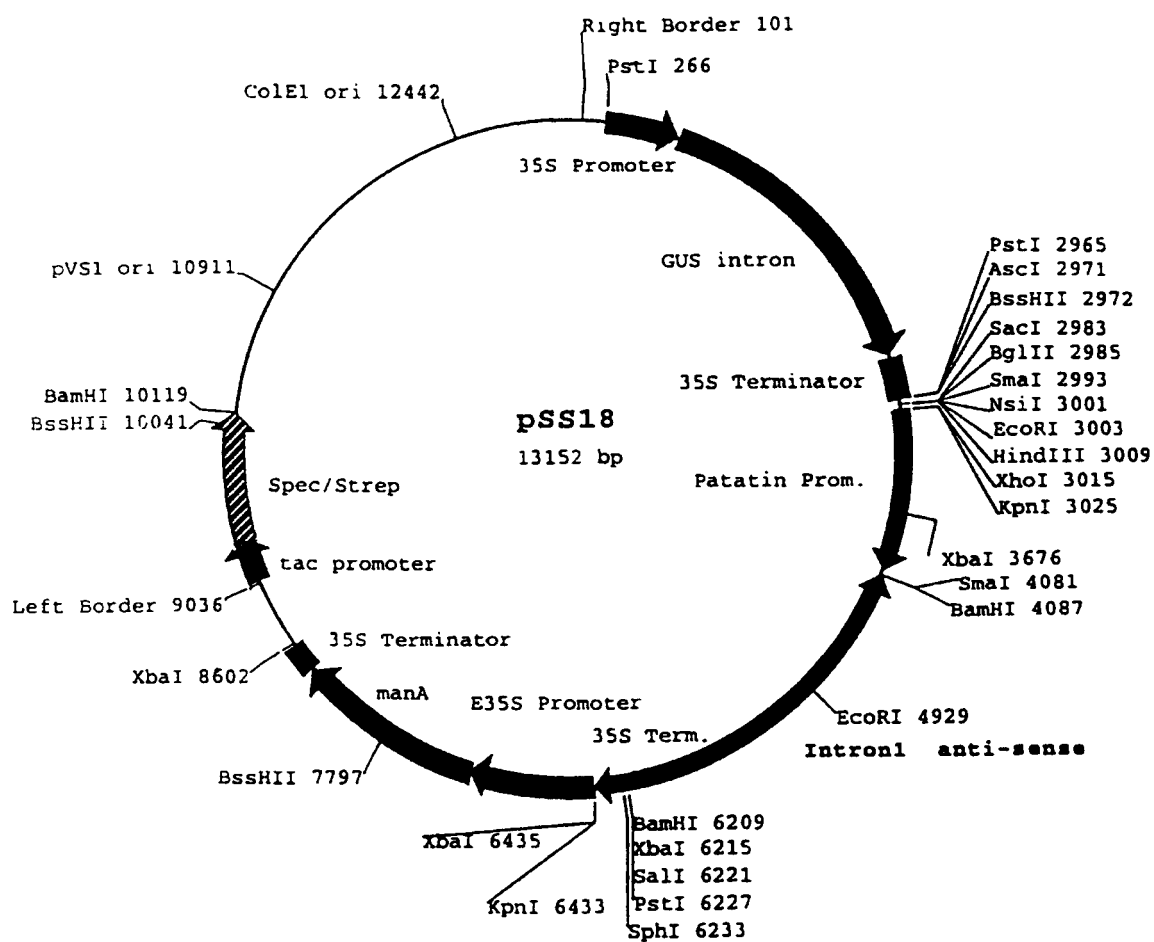


FIG. 16

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/00270

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N9/10 C12N15/11 C08B30/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C08B

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X	WO 97 04112 A (DANISCO ;POULSEN PETER (DK)) 6 February 1997 cited in the application see the whole document ---	1-21
X	WO 97 04113 A (DANISCO ;POULSEN PETER (DK)) 6 February 1997 cited in the application see the whole document ---	1-21
Y	WO 96 34968 A (NAT STARCH CHEM INVEST ;COOKE DAVID (GB); DEBET MARTINE (GB); GIDL) 7 November 1996 cited in the application see page 5, paragraph 3 - paragraph 4 see page 9, paragraph 2 - page 10, paragraph 1 ---	1-21
X	see page 11, paragraph 3 ---	17-19
-/--		



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents

"A" document defining the general state of the art which is not considered to be of particular relevance

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"&" document member of the same patent family

Date of the actual completion of the international search

29 May 1998

Date of mailing of the international search report

09/06/1998

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Authorized officer

Chakravarty, A

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/00270

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
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Y	WO 94 09144 A (ZENECA LTD) 28 April 1994 see page 10, line 1 - line 18 ---	1-21
Y	WO 92 15680 A (UNIV TEXAS) 17 September 1992 see page 6, line 17 - line 28 ---	1-21
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